

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2002, 16:22:51 ; Search time 29.94 Seconds
(without alignments)
467.445 Million cell updates/sec

Title: US-09-926-256-1
Perfect score: 699
Sequence: 1 DLECPGSMYSYDRYCYKPKF.....WFKVDCEDQHSHFCKFTKPR 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_032802:*

- 1: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
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- 5: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
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- 10: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*
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- 18: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	696	99.6	126	16	AA1979	Snake venom derivate
2	696	99.6	126	21	AA1985	Snake venom derivate
3	696	99.6	149	16	AA1981	Snake venom antith
4	696	99.6	149	21	AA1985	Snake venom derivate
5	673	96.3	127	13	AA1982	Snake venom derivate
6	348.5	49.9	130	14	AA1982	Snake venom derivate
7	330.5	47.3	131	14	AA1982	Snake venom derivate
8	330.5	47.3	132	14	AA1982	Snake venom derivate
9	323	46.2	133	14	AA1985	Snake venom derivate
10	319.5	45.7	134	14	AA1985	Snake venom derivate
11	300.5	43.0	152	22	AA1985	Snake venom derivate

12	265.5	38.0	132	16	AA1982	Snake venom derivate
13	264.5	37.8	133	14	AA1982	Snake venom derivate
14	255.5	36.6	123	14	AA1982	Snake venom derivate
15	233.5	33.4	127	16	AA1982	Snake venom derivate
16	222.5	31.8	146	22	AA1982	Snake venom derivate
17	221	31.6	116	13	AA1982	Snake venom derivate
18	220	31.5	38	16	AA1982	Snake venom derivate
19	212	30.3	107	14	AA1982	Snake venom derivate
20	209	29.9	36	13	AA1982	Snake venom derivate
21	203.5	29.1	125	14	AA1982	Snake venom derivate
22	200.5	28.7	125	14	AA1982	Snake venom derivate
23	187	26.8	166	9	AA1982	Snake venom derivate
24	185	26.5	165	10	AA1982	Snake venom derivate
25	181	25.9	133	15	AA1982	Snake venom derivate
26	181	25.9	144	15	AA1982	Snake venom derivate
27	181	25.9	146	15	AA1982	Snake venom derivate
28	181	25.9	147	11	AA1982	Snake venom derivate
29	181	25.9	166	15	AA1982	Snake venom derivate
30	181	25.9	166	22	AA1982	Snake venom derivate
31	181	25.9	166	22	AA1982	Snake venom derivate
32	181	25.9	174	21	AA1982	Snake venom derivate
33	176.5	25.3	175	15	AA1982	Snake venom derivate
34	174	24.9	165	14	AA1982	Snake venom derivate
35	172	24.6	44	21	AA1982	Snake venom derivate
36	171	24.5	50	13	AA1982	Snake venom derivate
37	169.5	24.2	175	11	AA1982	Snake venom derivate
38	169.5	24.2	175	20	AA1982	Snake venom derivate
39	169.5	24.2	175	21	AA1982	Snake venom derivate
40	167	23.9	173	14	AA1982	Snake venom derivate
41	166.5	23.8	175	15	AA1982	Snake venom derivate
42	166.5	23.8	175	15	AA1982	Snake venom derivate
43	166.5	23.8	183	21	AA1982	Snake venom derivate
44	162	23.2	43	16	AA1982	Snake venom derivate
45	162	23.2	165	10	AA1982	Snake venom derivate

ALIGNMENTS

RESULT 1	
ID	AA1979 standard; peptide; 126 AA.
AC	AA1979;
XX	
DT	28-NOV-1995 (first entry)
XX	
DE	Snake venom derived antithrombotic peptide.
XX	
KW	Antithrombotic peptide; snake venom; platelet binding inhibition; von Willebrand factors; Crotalus horridus horridus.
XX	
OS	Crotalus horridus horridus.
XX	
FH	Key
FT	Disulfide-bond 4..15
FT	Disulfide-bond 32..120
FT	Disulfide-bond 95..112
XX	
PN	W09508573-A.
XX	
PD	30-MAR-1995.
XX	
PF	21-SEP-1994; 94WO-JP01555.
XX	
PR	22-SEP-1993; 93JP-0236975.
XX	
PA	(AJTN) AJTNOMOTO KK.
XX	
PI	Fukuchi N, Ishii K, Kito M, Kobayashi T, Nagano M;
XX	Tanaka A, Yamamoto H, Yoshimoto R;
DR	WPI: 1995-139559/18.

Vigera palestinae
Sequence of polypeptide
Sequence of polypeptide
Vigera palestinae
Snake venom blood
Sequence of the pl
Snake venom derivate
Sequence of polypeptide
N-terminal sequenc
Botrocetin beta su
Sequence of polypeptide
Sequence encoded b
Human reg protein.
Human reg protein
Human reg protein
Human reg protein
Reg protein analog
Human reg protein.
Human colon associ
Human colon associ
Human cancer associ
Mouse PAP. Mus mu
MURBG-1. Mus musc
Snake venom derivate
N-terminal sequenc
Bovine pancreatic
Reg-2 protein. Ra
Amino acid sequenc
MURBG-2. Mus musc
Mouse PAP. Mus mu
Human pancreatilis
Human cancer associ
Vigera palestinae
Rat reg protein.

XX Single-chain antithrombotic peptide - obtained by cleaving an
PT oligopeptide from snake venom to break inter-chain di:sulphide
PT bonds but preserve intra-chain di:sulphide bonds
XX
PS Claim 3; Pages 44-45; 84pp; Japanese.
XX
XX AAR71978 and AAR71979 are snake venom derived antithrombotic
CC peptides, prepared by cleaving the interpeptide but retaining
CC the intrapeptide disulphide bonds of the original snake venom
CC oligopeptide. These peptides have the advantage of avoiding
CC significant thrombocytopenia when administered at the minimum
CC dose, for in vivo inhibition of platelet von Willebrand factor
CC binding.
XX
SQ Sequence 126 AA;

Query Match 99.6%; Score 696; DB 16; Length 126;
Best Local Similarity 99.2%; Pred. No. 3.8e-74;
Matches 125; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLECPGMSYDRYCYKPKFKQEMTMADAPRCSEQAKGHLSTETALEASFDNVLYAN 60
Db 1 dlecpqswssydrlycykpkfkqemtwaerfcseqakqghllsvetaleasfdvnllyan 60

QY 61 KEYLTRYIWIIGLRVONKQGPCSSISYENLVDPPECFMWSRDTRLREMFKYDCEQHSFIC 120
Db 61 keyltrylwiiglrvqnkqpcssisyenlvdpfecfmwsrdtrlrwfkvdcqghsfic 120

QY 121 KETRRP 126
Db 121 ketrpr 126

RESULT 2
ID AAR71981 standard; Protein; 126 AA.
XX
XX AAY85627;
XX
XX 07-FEB-2001 (first entry)
XX
XX Snake venom derived protein.
XX
XX Subunit peptide production; snake venom; rattlesnake; thrombolytic;
KW von Willebrand's factor; blood platelet-inhibitory activity.
XX
XX Crotales horridus horridus.
XX
XX WO200059926-A1.
XX
XX 12-OCT-2000.
XX
XX 31-MAR-2000; 2000WO-JP02127.
XX
XX 02-APR-1999; 99JP-0096073.
XX
XX (AJIN) AJINOMOTO CO INC.
XX
XX Fukuchi N, Kageyama S, Kito M, Kayahara T, Yamamoto H;
XX
XX WPI; 2000-664985/64.
XX
XX Producing physiologically-active subunit peptides originating in
PT polymer proteins by denaturation and specific separation, with lower
PT antigenicity but improved solubility and stability, e.g. blood
PT platelet-binding inhibitors -
XX
XX Claim 15; Page 44; 51pp; Japanese.
XX
XX This invention relates to a method for the production of a subunit
CC peptide originating from a polymer protein with disulphide bonds within

CC and between subunits. The method comprises denaturing the protein or its
CC subunit using a protein denaturing agent in a solution, removing the
CC agent in the presence of a polyoxalkyl polyether which reacts with a
CC thiol group and unwinds the subunit, and separating the polyoxalkyl
CC polyether-bound subunit peptide. The method can be used for producing
CC physiologically-active subunit peptides for polymer proteins e.g. snake
CC venom-originated dimer peptide with blood platelet-inhibitory activity
CC on von Willebrand's factor. The peptides produced have platelet-binding
CC inhibitory, and thrombolytic activity. The present sequence represents a
CC rattle snake protein used in an example illustrating the method of the
XX
XX
SQ Sequence 126 AA;

Query Match 99.6%; Score 696; DB 21; Length 126;
Best Local Similarity 99.2%; Pred. No. 3.8e-74;
Matches 125; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLECPGMSYDRYCYKPKFKQEMTMADAPRCSEQAKGHLSTETALEASFDNVLYAN 60
Db 1 dlecpqswssydrlycykpkfkqemtwaerfcseqakqghllsvetaleasfdvnllyan 60

QY 61 KEYLTRYIWIIGLRVONKQGPCSSISYENLVDPPECFMWSRDTRLREMFKYDCEQHSFIC 120
Db 61 keyltrylwiiglrvqnkqpcssisyenlvdpfecfmwsrdtrlrwfkvdcqghsfic 120

QY 121 KETRRP 126
Db 121 ketrpr 126

RESULT 3
ID AAR71981 standard; Protein; 149 AA.
XX
XX AAR71981;
XX
XX 28-NOV-1995 (first entry)
XX
XX Snake venom antithrombotic oligopeptide.
XX
XX Antithrombotic peptide; snake venom; platelet binding inhibition;
KW von Willebrand factors; Crotales horridus horridus.
XX
XX Crotales horridus horridus.
XX
XX
FH Key Location/Qualifiers
FT Disulfide-bond 27..38
FT Disulfide-bond 55..143
FT Disulfide-bond 118..135
XX
XX WO9508573-A.
XX
XX 30-MAR-1995.
XX
XX 21-SEP-1994; 94WO-JP01555.
XX
XX 22-SEP-1993; 93JP-0236975.
XX
XX (AJIN) AJINOMOTO KK.
XX
XX Fukuchi N, Ishii K, Kito M, Kobayashi T, Nagano M;
PI Tanaka A, Yamamoto H, Yoshimoto R;
XX
XX WPI; 1995-139559/18.
XX
XX N-PSDB; AAQ89309.
XX
XX Single-chain antithrombotic peptide - obtained by cleaving an
PT oligopeptide from snake venom to break inter-chain di:sulphide
PT bonds but preserve intra-chain di:sulphide bonds
XX
XX Example 2; Pages 47-48; 84pp; Japanese.

XX AAR71978 and AAR71979 are snake venom derived antithrombotic peptides,
 CC specifically from the snake venom oligopeptide AAR71981, encoded by
 CC AA089309. These peptides have the advantage of avoiding significant
 CC thrombocytopenia when administered at the minimum dose, for in vivo
 CC inhibition of platelet von Willebrand factor binding.

XX Sequence 149 AA:

Query Match 99.6%; Score 696; DB 16; Length 149;
 Best Local Similarity 99.2%; Pred. No. 4.7e-74;
 Matches 125; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLECPGSSSYDRYCYKPKPKQEMTWDAQRFCSQAQKGGHLSVETALASFDVNYLYAN 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 24 dlecpssgsysdyrcykpkpkqemtwaerfcsegakgghllsvetaleasfdvnylyan 83
 OY 61 KEYLFRYIWIGLRVONKGGPCSSISYENLVDPPECFMWSRDTLRWFVKVDCQOHSFTC 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 84 keylfrlywiglrvgnkqgpcssisye nlvdpfecfmwsrdtrlrwfkvdceqghsfic 143
 OY 121 KFTRRR 126
 |||||||
 Db 144 kftrrp 149

RESULT 4

AA85628
 ID AAY85628 standard; protein; 149 AA.

XX AAY85628;

DT 07-FEB-2001 (first entry)

DE Snake venom derived protein.

XX Subunit peptide production; snake venom; rattlesnake; thrombolytic;

KW von Willebrand's factor; blood platelet-inhibitory activity.

XX Crotales horridus horridus.

PN WO200059926-A1.

PD 12-OCT-2000.

PF 31-MAR-2000; 2000WO-JP02127.

PR 02-APR-1999; 99JP-0096073.

XX (AJIN) AJINOMOTO CO INC.

PI Fukuchi N, Kageyama S, Kito M, Kayahara T, Yamamoto H;

DR WPI: 2000-664985/64.
 N-PSDB; AAC61144.

XX Producing physiologically-active subunit peptides originating in
 PT polymer proteins by denaturation and specific separation, with lower
 PT antigenicity but improved solubility and stability, e.g. blood
 PT platelet-binding inhibitors -

XX Example 2; Page 47; 51pp; Japanese.

XX This invention relates to a method for the production of a subunit
 CC peptide originating from a polymer protein with disulphide bonds within
 CC and between subunits. The method comprises denaturing the protein or its
 CC subunit using a protein denaturing agent in a solution, removing the
 CC agent in the presence of a polyoxalkyl polyether which reacts with a
 CC thiol group and unwinds the subunit, and separating the polyoxalkyl
 CC polyether-bound subunit peptide. The method can be used for producing
 CC physiologically-active subunit peptides for polymer proteins e.g. snake
 CC venom-originated dimer peptide with blood platelet-inhibitory activity

CC on von Willebrand's factor. The peptides produced have platelet-binding
 CC inhibitory, and thrombolytic activity. The present sequence represents a
 CC rattlesnake protein used in an example illustrating the method of the
 CC invention.

XX Sequence 149 AA:

Query Match 99.6%; Score 696; DB 21; Length 149;
 Best Local Similarity 99.2%; Pred. No. 4.7e-74;
 Matches 125; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DLECPGSSSYDRYCYKPKPKQEMTWDAQRFCSQAQKGGHLSVETALASFDVNYLYAN 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 24 dlecpssgsysdyrcykpkpkqemtwaerfcsegakgghllsvetaleasfdvnylyan 83
 OY 61 KEYLFRYIWIGLRVONKGGPCSSISYENLVDPPECFMWSRDTLRWFVKVDCQOHSFTC 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 84 keylfrlywiglrvgnkqgpcssisye nlvdpfecfmwsrdtrlrwfkvdceqghsfic 143
 OY 121 KFTRRR 126
 |||||||
 Db 144 kftrrp 149

RESULT 5

AA24426
 ID AAR24426 standard; Protein; 127 AA.

XX AAR24426;

DT 21-NOV-1992 (first entry)

DE Sequence of the platelet glycoprotein GPIb inhibitor alpha chain
 (CHH-B-alpha).

KW Platelet adherence inhibitor; platelet anti-adhesive;

KW antithrombotic agent; von Willebrand factor;

KW platelet glycoprotein GPIb-IX complex.

XX Crotales horridus horridus.

PN WO9208472-A.

PD 29-MAY-1992.

PF 14-NOV-1991; 91WO-US08516.

PR 16-NOV-1990; 90US-0614443.

XX (CORT-) COR THERAPEUTICS INC.

PI Scarborough RM;

DR WPI: 1992-199936/24.

XX Platelet antiadhesive peptide(s) obtd. from snake venom - also
 PT inhibit thrombus formation; for treatment of arteriosclerosis,
 PT atherosclerosis, acute myocardial infarction, chronic unstable
 PT angina, etc.

XX Example; Fig 6; 5pp; English.

XX The PAA was purified from a solution of snake venom. Analysis of
 CC the peak inhibitory fractions by SDS-PAGE revealed 2 major proteins
 CC migrating with a mol. wt. 23-28 kD. Both were able to inhibit
 CC botrocetin and ristocetin induced platelet agglutination. They were
 CC called CHH-A and CHH-B. The earlier eluting subunit (CHH-B-beta)
 CC and later eluting subunit (CHH-B-alpha) were individually submitted
 CC to N-terminal sequence analysis. The complete amino acid sequence
 CC for the alpha and beta chains are given in AAR24426 and AAR24427.

XX Sequence 127 AA:

PR	05-JUN-1992;	92US-0893929.
XX	(UTEM) UNIV TEMPLE.	
PA		
XX		
PI	Kirby EP, Peng M;	
XX		
DR	WPI; 1993-196991/24.	
XX		
PT	New platelet-binding proteins obtained from snake venom - inhibit	
PT	binding of von Willebrand factor to platelet membrane	
PT	glycoprotein IB, useful in therapy, diagnosis and surgery	
XX		
XX		
PS	Claim 4; Page 46; 74pp; English.	
XX		
CC	Al-A may be obt. from snake venom. It has a mol. wt. of about 45	
CC	kDa. Al-A contains two types of polypeptide chains, with mol. wt. of	
CC	about 18 kDa and about 15 kDa, respectively. Each of these two types	
CC	of chains is actually composed of two subtypes. Thus, Al-A comprises	
CC	four non-identical polypeptide chains. A possible variation of	
CC	AA388224 has been found, characterised by Asp at posn. three in lieu	
CC	of Cys.	
XX		
XX		
Sequence	134 AA;	
XX		

Query Match	45.7%;	Score	319.5;	DB	14;	Length	134;
Best Local Similarity	42.7%;	Pred. No.	1e-29;				
Matches	56;	Conservative	27;	Mismatches	39;	Indels	9;
						Gaps	2;

```
QY      DLBEPSSWSSDPRCXPYPFQOEMTMAADPSCSOAGCHILSTETLAEASFUNDNYXAN 60
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      dfncfpagssdqcyvrfnephkmedaeefcaqgaasghlvstetngeedffvaqlsen 60
QY      61 KEYLTRITIMIGLRNQNGQPC-----SSTSYNLVDPF--ECFMWSRQTRLREMKVD 111
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 lqskehvvwjdliknkeqqcgsseswdgsavlyealliklmyrkcgalesgdfkwkwlj 120
QY      112 GEQHSHFTCKE 122
        | : |||
Db      121 cldqnpfycfe 131
```

XX	RESULT	11
XX	AAAM51543	
XX	ID	AAAM51543 standard; Protein: 152 AA.
XX	AC	AAAM51543;
XX	DT	10-JAN-2002 (first entry)
XX	DE	Snake venom blood anticoagulant halysin A chain.
XX	KW	Snake; pit viper; venom; halysin; anticoagulant; thrombogenesis;
XX	KM	thrombosis.
XX	OS	Agkistrodon halys.
XX	PN	KR2001049671-A.
XX	PD	15-JUN-2001.
XX	PF	29-JUN-2000; 2000KR-0036591.
XX	PR	29-JUN-1999; 99KR-0025105.
XX	PA	(BIOB-) BIOBUD CO LTD.
XX	PI	Jang YS, Jung GH, Kim DS, Koo BH, Son YD;
XX	WPI	2001-637330/73.
XX	DR	N-PSDB; AAI71876.
XX	TX	Halysin as blood anticoagulation protein separated from snake venom -

xx Claim 2: Page 10; 21pp. Korean.
 ps
 xx
 CC The invention relates to halyxin, a novel protein with very strong
 CC blood anticoagulation activity. The protein was separated from snake
 CC venom of *Akistrodon halys brevicaudus* (a Korean pit viper) and can
 CC be used in the treatment of thrombogenesis. The present sequence
 CC is the A chain of halyxin.
 xx
 SQ Sequence 152 AA:

Query Match	43.0%;	Score	300.5;	DB	22;	Length	152;
Best Local	Similarly	41.4%;	Pred.	No. 2.2e-27;			
Matches	53;	Conservative	29;	Mismatches	37;	Indels	9;
						Gaps	2;

[illegible]

QY 63 YLTRYIWIGLRVQNKQPC-----SSISYENLVDPFE--CFMSRDTLRLEMFKYDCE 113
 |||||: : : : 11:|: : : : : : : : : :
 Db 84 rygiylwiiglrivrgkkqcgssgwsdgsyrygnwleanskctlgiketeftkwnfygc 143

QY	114	QQHSFICK	121
		::: 1::1:	
Db	144	ernpfvce	151

RESULT	12
AAR72235	
ID	AAR72235 standard; peptide; 132 AA.

AC	AA72235;
XX	
DT	04-DEC-1995 (first entry)
XX	
DE	Vipera palestinae venom derived peptide.
XX	
KW	Vipera palestinae; venom; antithrombotic agent; platelet binding; von Willebrand factor.
XX	
OS	Vipera palestinae.
XX	
PN	W09509183-A.
XX	
PD	06-APR-1995.
XX	
PF	27-SEP-1994; 94WO-JP01583.
XX	
PR	28-SEP-1993; 93JP-0241666.
PR	14-JAN-1994; 94JP-0002691.
XX	10-JUN-1994; 94JP-0128518.
PA	(AJIN) AJINOMOTO KK.
XX	
PI	Fukuchi N, Ishii K, Kaida K, Kobayashi T;
XX	
DR	WPI: 1995-147392/19.
XX	
PT	Peptide derived from Vipera palestinae venom - inhibits binding of platelets to von Willebrand factor, useful as antithrombotic agent
XX	
PS	Claim 5; Page 19; 37pp; Japanese.
XX	
CC	AA72235 is a Vipera palestinae venom derived peptide. A peptide composn. comprising AA72235 and AA72236 is claimed, it inhibits the binding of platelets to von Willebrand factors and can therefore be used as an anti- thrombotic agent.
CC	
XX	
SQ	Sequence 132 AA;

	Query Match	38.0%; Score 265.5; DB 16; Length 132;
	Best Local Similarity	39.1%; Pred. No. 2.4e-23;
	Matches 50; Conservative	25; Mismatches 46; Indels 7; Gaps 1.
OY	1 DLECGSGMSVDRYCYKPKFKOEMTWADAQRFCSSECAKGSHLISVETALEASFPDVNYLAN 60 I : : : : : : :	Dd 1 dgdcdpsdssshneghcyrkfrlftkeeeakctmqgynghlasiesveeanltvaelvskt 60
OY	61 KEYLTRYIWGLRVONKQCPCSS-----ISENIVDFEFCFNVSRDTRLREWEKVDC 113 : : : : : :	Dd 61 llskxyhawigjrdserqgcshwtsgsavseyeltvckycfglnkdkgylewvtlpoe 120
OY	114 QGHSPICK 121 :	
Dd	121 dkpflick 128	
	RESULT 13	
ID	AAR38230	
	AAR38230 standard; protein; 133 AA.	
XX	AAR38230;	
AC	AAAR38230;	
XX	01-OCT-1993 (first entry)	
DT	Sequence of polypeptide chain of alboaggregin-like protein called echicetin.	
DE	Venom; snake; platelet-binding protein.	
XX	Echis carinatus.	
XOS	WO9311151-A.	
FN	10-JUN-1993.	
PD	01-DEC-1992; 92MO-US10344.	
PF	03-DEC-1991; 91US-0803630.	
PR	05-JUN-1992; 92US-0893929.	
XX	(UTEM) UNIT TEMPLE.	
PA	Kirby EP, Peng M;	
Pt	WPI; 1993-196991/24.	
DR	New platelet-binding proteins obtained from snake venom - inhibit binding of von Willebrand factor to platelet membrane	
XX	* glycoprotein IB, useful in therapy, diagnosis and surgery	
PS	Claim 10; Page 49; 74pp; English.	
CC	Echicetin, is obtained in substantially pure chemical form from venom, as an about 26 kDa protein which likely comprises a dimer composed of two types of chains. One chain type has a mol. wt. of about 15 kDa and the other has a mol. wt. of about 13 kDa. The individual polypeptide chains are held together by one or more interchain disulfide bonds.	
CC	Sequence 133 AA;	
SQ	Query Match 37.8%, Score 264.5; DB 14; Length 133; Best Local Similarity 37.8%; Pred. No. 3.2e-23; Matches 51; Conservative 32; Mismatches 41; Indels 11; Gaps 4.	
OY	1 DLECGSGMSVDRYCYKPKFKOEMTWADAQRFCSSECAKGSHLISVETALEASFPDVNYLAN 60 I : : : : : : :	Dd 1 dgdcdgsfyeghegyqlfrik-twdeaeekychn-qwdggghlvstiesnakaetvraqllsrk 58
OY	61 --KEYLTRYIWGLRVONKQCPC-----SISIVENLVDPFECPMVNSHRTLREWFKYD 111	

Dd		59	pkasiedrwtw gldrdrcqegcghlwtcdnsivhyehvnpptcktlvlerqtcefirwiavn	118
OY		112	CEQOHSFTCKFTRPR	126
Dd		119	cefkfpfcvkakipr	133
 RESULT_14				
ID	AAR38225		standard; protein; 123 AA.	
XX	AAR38225;			
XX				
DT	01-OCT-1993	(first entry)		
XX				
DE			Sequence of polypeptide chain of alboaagregin A (Al-A).	
XX				
KW	Venom; snake; platelet-binding protein.			
OS	Trimeresurus albolarbris.			
PX	WO9311151-A.			
XX				
PD	10-JUN-1993.			
XX				
PF	01-DEC-1992;	92WO-US10344.		
XX				
PR	03-DEC-1991;	91US-0803630.		
PR	05-JUN-1992;	92US-0893929.		
XX				
PA	(UTEM) UNIV TEMPLE.			
XX				
PI	Kirby EP, Peng M;			
XX				
DR	WPT:1993-196991/24.			
XX				
PT	New platelet-binding proteins obtained from snake venom - inhibit			
PT	binding of von Willebrand factor to platelet membrane			
PT	glycoprotein IB, useful in therapy, diagnosis and surgery			
XX				
PS	Claim 4; Page 47; 74pp; English.			
CC	Al-A may be obt'd. from snake venom. It has a mol. wt. of about 45			
CC	kDa. Al-A contains two types of polypeptide chains, with mol. wt. of			
CC	about 18 kDa and about 15 kDa, respectively. Each of these two types			
CC	of chains is actually composed of two subtypes. Thus, Al-A comprises			
CC	four non-identical polypeptide chains. A possible variation of			
CC	AAR38224 has been found, characterised by asp at posn. three in lieu			
CC	of Cys.			
XX				
SQ	Sequence	123 AA;		
 Query Match				
	Similarity	36.6%;	Score 255.5;	DB 14; Length 123;
Best Local	Conservative	23;	Mismatches 35;	Indels 21; Gaps 6;
OY	3 ECPGSMSSYDRRCYAPFKOEWTADQRFCSEDAKGGHLSVETALAESFYDN---VLV	58		
Dd	1 dpdsdwasyeghcycyvfnepqmwadaekfctqhgshlsfsgsgadfvvmtrplln	60		
OY	59 ANKEVLTRYITWGLRNVQNGQPCSS-----ISTENLVDPPECFMWSRDDRLRKREFKVD	111		
Dd	61 an-----lwvlgl--snlmwcnsqwsdgtxldykxwrqfec-lvarltln-newlsmd	110		
OY	112 CEQOHSFTCKF	122		
Dd	111 cssthsfvcf	121		
 RESULT_15				
AAR72236				

```

ID AAR72236 standard; peptide: 127 AA.
XX
AC AAR72236;
XX
DT 04-DEC-1995 (first entry)
XX
DE Vipera palestinae venom derived peptide.
XX
KW Vipera palestinae; venom; antithrombotic agent;
XX platelet binding; von Willebrand factor.
OS Vipera palestinae.
XX
PN WO9509183-A.
XX
PD 06-APR-1995.
XX
PF 27-SEP-1994; 94WO-JP01583.
XX
PR 28-SEP-1993; 93JP-0241666.
PR 14-JAN-1994; 94JP-0002691.
PR 10-JUN-1994; 94JP-0128518.
XX
PA (AJIN ) AJINOMOTO KK.
XX
PI Fukuchi N, Ishii K, Kaide K, Kobayashi T;
XX
DR WPI; 1995-147392/19.
XX
PT Peptide derived from Vipera palestinae venom - inhibits binding
PT of platelets to von Willebrand factor, useful as antithrombotic
PT agent
XX
PS Claim 5; Pages 19-20; 37pp; Japanese.
XX
CC AAR72236 is a Vipera palestinae venom derived peptide. A peptide
CC compsn. comprising AAR72235 and AAR72236 is claimed, it inhibits the
CC binding of platelets to von Willebrand factors and can therefore
CC be used as an anti- thrombotic agent.
XX
SQ Sequence 127 AA;

Query Match 33.4%; Score 233.5; DB 16; Length 127;
Best Local Similarity 36.6%; Pred. No. 1.4e-19;
Matches 48; Conservative 25; Mismatches 45; Indels 13; Gaps 4;

QY 3 ECPSCGSSYDRCYKPKPEKQEWMTADAOFCSEOKGCHLSVETALEASFVNVLYANKE 62
   :||| |||:::||| | : |||||::|:| | |||||::| : : : : :
DB 1 dcpsdwsshnegncykvfnidctwadaekfctegvsgghlslskstevdffmklivpilk 60
   :||| |||:::||| | : |||||::|:| | |||||::| : : : : :
QY 63 YLTRYIMIGLRVONKGGPCS-----SISYENLVDPFCECFMVSRTRLREWFKYDCEQ 115
   | ||||| | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 61 y--dlwlgf--snfwrdcnwgwsgvklidykawsdipdcyvak--twdygwllrdcst 114
   : |||| | |
QY 116 HSFICKFTPR 126
   : |||| | |
DB 115 yflicksrivr 125

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Search completed: October 3, 2002, 16:24:50
 Job time: 119 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2002, 16:23:06 ; Search time 12.89 Seconds

(without alignments)
238.761 Million cell updates/sec

Title: US-09-926-256-1

Perfect score: 699
Sequence: 1 DLECPGSGSSYDRYCKPKF.....WFKVDEQGHSTCKTTPR 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PC10S.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfill1est.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	99.6	126	2	US-08-612-840A-2
2	696	99.6	149	2	US-08-612-840A-8
3	673	96.3	127	1	US-07-614-443A-1
4	673	96.3	127	1	US-08-294-859-1
5	673	96.3	127	1	US-08-481-676-1
6	348.5	49.9	130	1	US-07-893-929A-7
7	348.5	49.9	130	5	PCT-US92-10344-9
8	338.5	48.4	131	1	US-07-893-929A-1
9	338.5	48.4	131	5	PCT-US92-10344-1
10	333.5	47.7	132	1	US-07-893-929A-5
11	333.5	47.7	132	5	PCT-US92-10344-5
12	319.5	45.7	134	1	US-07-893-929A-2
13	319.5	45.7	134	5	PCT-US92-10344-2
14	264.5	37.8	133	1	US-07-893-929A-9
15	264.5	37.8	133	5	PCT-US92-10344-9
16	264.5	37.7	123	1	US-07-893-929A-4
17	263.5	37.7	123	5	PCT-US92-10344-4
18	223.5	32.0	117	1	US-07-614-443A-2
19	223.5	32.0	117	1	US-08-294-859-2
20	223.5	32.0	117	1	US-08-481-676-2
21	220	31.5	38	2	US-08-612-840A-1
22	212	30.3	107	1	US-07-893-929A-6
23	212	30.3	107	5	PCT-US92-10344-6
24	200.5	28.7	125	1	US-07-893-929A-3
25	200.5	28.7	125	1	PCT-US92-10344-3
26	174.5	25.0	175	2	US-08-401-530A-3
27	174.5	25.0	175	2	US-08-709-662-3

28	171	24.5	50	1	US-07-614-443A-5	Sequence 5, Appl1
29	171	24.5	50	1	US-08-294-859-5	Sequence 5, Appl1
30	171	24.5	50	1	US-08-481-676-5	Sequence 10, Appl1
31	170	24.3	123	1	US-07-893-929A-10	Sequence 10, Appl1
32	170	24.3	123	5	PCT-US92-10344-10	Sequence 10, Appl1
33	166.5	23.8	175	2	US-08-464-637-2	Sequence 2, Appl1
34	166.5	23.8	175	2	US-08-401-530A-4	Sequence 4, Appl1
35	166.5	23.8	175	2	US-08-709-662-4	Sequence 4, Appl1
36	166.5	23.8	175	2	US-08-822-261-3	Sequence 3, Appl1
37	161.5	23.1	175	2	US-08-822-261-1	Sequence 4, Appl1
38	160.5	23.0	128	1	US-07-893-929A-8	Sequence 8, Appl1
39	160.5	23.0	128	5	PCT-US92-10344-8	Sequence 8, Appl1
40	160	22.9	165	2	US-08-401-530A-7	Sequence 7, Appl1
41	160	22.9	165	2	US-08-729-103-3	Sequence 3, Appl1
42	160	22.9	165	2	US-08-709-662-7	Sequence 7, Appl1
43	160	22.9	166	2	US-08-729-103-4	Sequence 4, Appl1
44	155.5	22.2	174	1	US-07-778-156-7	Sequence 7, Appl1
45	155.5	22.2	174	2	US-08-822-261-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-612-840A-2
; Sequence 2, Application US/08612840A
; Patent No. 5856126
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, Naoyuki
; APPLICANT: YAMAMOTO, Hitoshi
; APPLICANT: NAGANO, Mitsuyo
; APPLICANT: KITAO, Morikazu
; APPLICANT: TANAKA, Akiko
; APPLICANT: ISHII, Koichi
; APPLICANT: KOBAYASHI, Tsuyoshi
; APPLICANT: YOSHIMOTO, Ryota
; TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
; TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Obion, Spivak, Mclelland, Maier & Neustadt, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,840A
; FILING DATE: 20-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-236975
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5856126man F. Obion
; REGISTRATION NUMBER: 24,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-612-840A-2

Query Match 99.6%; Score 696; DB 2; Length 126;
Best Local Similarity 99.2%; Pred. No. 7.7e-79;
Matches 125; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEDAKGGHLLSVETALEASFVNDVLYAN 60
|||||
DB 1 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEDAKGGHLLSVETALEASFVNDVLYAN 60
|||||

QY 61 KEYLTRYIWIIGLRYONKQPCSSISENLVDPFECFVNSRDTRLREMFKVDCEQOHSFIC 120
|||||
DB 61 KEYLTRYIWIIGLRYONKQPCSSISENLVDPFECFVNSRDTRLREMFKVDCEQOHSFIC 120
|||||

QY 121 KETRRP 126
|||||
DB 121 KETRRP 126

RESULT 2
US-08-612-840A-8
; Sequence 8, Application US/08612840A
; Patent No. 5856126
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, Naoyuki
; APPLICANT: YAMAMOTO, Hiroshi
; APPLICANT: NAGANO, Mitsuyo
; APPLICANT: KITO, Morikazu
; APPLICANT: TANAKA, Akiko
; APPLICANT: ISHII, Koichi
; APPLICANT: KOBAYASHI, Tsuyoshi
; APPLICANT: YOSHIMOTO, Ryota
; TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
; TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,840A
; FILING DATE: 20-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-236975
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5856126man F. Oblon
; REGISTRATION NUMBER: 24,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-840A-8

Query Match 99.6%; Score 696; DB 2; Length 149;
Best Local Similarity 99.2%; Pred. No. 9.7e-79;
Matches 125; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEDAKGGHLLSVETALEASFVNDVLYAN 60
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DB 24 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEDAKGGHLLSVETALEASFVNDVLYAN 83
QY 61 KEYLTRYIWIIGLRYONKQPCSSISENLVDPFECFVNSRDTRLREMFKVDCEQOHSFIC 120
|||||
DB 84 KEYLTRYIWIIGLRYONKQPCSSISENLVDPFECFVNSRDTRLREMFKVDCEQOHSFIC 143
QY 121 KETRRP 126
|||||
DB 144 KETRRP 149

RESULT 3
US-07-614-443A-1
; Sequence 1, Application US/07614443A
; Patent No. 5342830
; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/614,443A
; FILING DATE: 19901116
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22803-20003.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-614-443A-1

Query Match 96.3%; Score 673; DB 1; Length 127;
Best Local Similarity 96.8%; Pred. No. 5.6e-76;
Matches 122; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEDAKGGHLLSVETALEASFVNDVLYAN 60
|||||
DB 1 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEDAKGGHLLSVETALEASFVNDVLYAN 60
|||||

QY 61 KEYLTRYIWIIGLRYONKQPCSSISENLVDPFECFVNSRDTRLREMFKVDCEQOHSFIC 120
|||||
DB 61 KEYLTRYIWIIGLRYONKQPCSSISENLVDPFECFVNSRDTRLREMFKVDCEQOHSFIC 120
|||||

QY 121 KETRRP 126
|||||
DB 121 KETRRP 126

RESULT 4
US-08-294-859-1
; Sequence 1, Application US/08294859
; Patent No. 5679542

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; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1888
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,859
; FILING DATE: 29-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2803-0003.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
;
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-294-859-1
;
;
; Query Match          96.3%; Score 673; DB 1; Length 127;
; Best Local Similarity 96.8%; Pred. No. 5.6e-76;
; Matches 122; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
;
; QY 1 DLPCPSGWSYDRCYKPFKQEMTWADQRCSEQAKGHLSTVETALASVFNVLN 60
;      |||||||
; DB 1 DLPCPSGWSYDRCYKPFKQEMTWADQRCSEQAKGHLSTVETALASVFNVLN 60
;
; QY 61 KEYLTRIWIIGLRVQNGKQPCSSISYENLVDPFECFMYSRDTRLREMFKVDCEQHSFIC 120
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; DB 61 KEYLTRIWIIGLRVQNGKQPCSSISYENLVDPFECFMYSRDTRLREMFKVDCEQHSFIC 120
;
; QY 121 KFTRRP 126
;      |||||
; DB 121 KFTRRP 126
;
; RESULT 5
; US-08-481-676-1
; Sequence 1, Application US/08481676
; Patent No. 5744584
; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1888
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/481,676
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/294,859
; FILING DATE: 29-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2803-0003.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
;
; INFORMATION FOR SEQ. ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-481-676-1
;
;
; Query Match          96.3%; Score 673; DB 1; Length 127;
; Best Local Similarity 96.8%; Pred. No. 5.6e-76;
; Matches 122; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
;
; QY 1 DLPCPSGWSYDRCYKPFKQEMTWADQRCSEQAKGHLSTVETALASVFNVLN 60
;      |||||||
; DB 1 DLPCPSGWSYDRCYKPFKQEMTWADQRCSEQAKGHLSTVETALASVFNVLN 60
;
; QY 61 KEYLTRIWIIGLRVQNGKQPCSSISYENLVDPFECFMYSRDTRLREMFKVDCEQHSFIC 120
;      |||||||
; DB 61 KEYLTRIWIIGLRVQNGKQPCSSISYENLVDPFECFMYSRDTRLREMFKVDCEQHSFIC 120
;
; QY 121 KFTRRP 126
;      |||||
; DB 121 KFTRRP 126
;
; RESULT 6
; US-07-893-929A-7
; Sequence 7, Application US/07893929A
; Patent No. 533667
; GENERAL INFORMATION:
; APPLICANT: Kirby, Edward P.
; TITLE OF INVENTION: Alboagregins: Platelet
; TITLE OF INVENTION: Agonists Which Bind To Platelet
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of the Common-
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette, 3.50 inch, 720 kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/893,929A
; FILING DATE: 19920605
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/803,630
; FILING DATE: December 3, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5336667e
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-893-929A-7

Query Match
Best Local Similarity 49.9%; Score 348.5; DB 1; Length 130;
Matches 66; Conservative 24; Mismatches 27; Indels 13; Gaps 4;

QY 3 ECPGSSSYDRYCYKPFQEMTWADQRCFCEQAKGGHLLSVETALASFDVNLVYAN-K 61
:|||||:|||||:|:|||||:|||||:|:|:|:|
Db 1 DCPDWSFRCYQCYIVKELKTWEDAEFCSEQANDGHLVSIESTREAVFVALLSENVK 60
:|:|||||:|||||:|:|||||:|:|||||:|:|:|:|

QY 62 EYLRIRYIWLGRVQNKGPC-----SSISYENLV--DPFECFVNSRDTLRREMFVDC 112
:|:|||||:|||||:|:|||||:|:|||||:|:|:|:|
Db 61 KY--HWVIGLSYQNKGGQCSSEWSDSSVSYENLVKPNPKCFVLKKESEFKTWSNVYC 117
:|:|||||:|||||:|:|||||:|:|||||:|:|:|:|

QY 113 EQHSHFICKF 122
:|:|:|:|:|:|
Db 118 EQKHIFMCKF 127
:|:|:|:|:|:|

RESULT 7
PCT-US92-10344-7
Sequence 7, Application PC/TUS9210344
GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists which Bind To Platelet
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: AMINO ACID

TOPOLOGY: linear
PCT-US92-10344-7

Query Match
Best Local Similarity 49.9%; Score 348.5; DB 5; Length 130;
Matches 66; Conservative 24; Mismatches 27; Indels 13; Gaps 4;

QY 3 ECPGSSSYDRYCYKPFQEMTWADQRCFCEQAKGGHLLSVETALASFDVNLVYAN-K 61
:|||||:|||||:|:|||||:|||||:|:|:|:|
Db 1 DCPDWSFRCYQCYIVKELKTWEDAEFCSEQANDGHLVSIESTREAVFVALLSENVK 60
:|:|||||:|||||:|:|||||:|:|||||:|:|:|:|

QY 62 EYLRIRYIWLGRVQNKGPC-----SSISYENLV--DPFECFVNSRDTLRREMFVDC 112
:|:|||||:|||||:|:|||||:|:|||||:|:|:|:|
Db 61 KY--HWVIGLSYQNKGGQCSSEWSDSSVSYENLVKPNPKCFVLKKESEFKTWSNVYC 117
:|:|||||:|||||:|:|||||:|:|||||:|:|:|:|

QY 113 EQHSHFICKF 122
:|:|:|:|:|:|
Db 118 EQKHIFMCKF 127
:|:|:|:|:|:|

RESULT 8
US-07-893-929A-1
Sequence 1, Application US/07893929A
Patent No. 5336667
GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists which Bind To Platelet
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/893,929A
FILING DATE: 19920605
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5336667e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-893-929A-1

Query Match
Best Local Similarity 48.4%; Score 338.5; DB 1; Length 131;
Matches 62; Conservative 21; Mismatches 39; Indels 9; Gaps 2;

QY 3 ECPGSSSYDRYCYKPFQEMTWADQRCFCEQAKGGHLLSVETALASFDVNLVYANKE 62

```

Db      1 DCPDMSWDYDCYRVRFRRLQTMEDAEERFCSEQANDGHVLSIESAGCEADFTQLVSENIR    60
Oy      63 YLTRIWTIGLRYONKGPC-----SSISTENLYD--PECFMWSRPTRLREMPKYDCE    113
Db      61 SEKHVWVGILRVQOKGQCDSSEMSDGSSVHYHDLNDEKNTKRRCYGLEKRAEPRFTWSNVYCG    120
Oy      114 QOHSEICKEFTR 124
Db      121 HEYFPVCKEFXR 131

RESULT          9
PCT-US92-10344-1
Sequence 1, Application PC/TUS9210344
GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
TITLE OF INVENTION: Alboagregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
ADDRESSSEE: wealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19122

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIF) 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US92-10344-1

Query Match           48.4%; Score 338.5; DB 5; Length 131;
Best Local Similarity 47.3%; Pred. No. 1.8e-34;
Matches   62; Conservative 21; Mismatches 39; Indels   9; Gaps 22

Oy      3 RCPGSWSSYDRCYCPFEQEMTWAAORPCSOAKGGHLLSVETALASFYOVNLVANKE 62
Db      1 DCPDMSWSDYDCYRVRFRRLQTMEDAEERFCSEQANDGHVLSIESAGCEADFTQLVSENIR 60
Oy      63 YLTRIWTIGLRYONKGPC-----SSISTENLYD--PECFMWSRPTRLREMPKYDCE 113
Db      61 SEKHVWVGILRVQOGQQCSSSEMSDGSSVHYHDLNDEKNTKRRCYGLEKRAEPRFTWSNVYCG 120
Oy      114 QOHSEICKEFTR 124
Db      121 HEYFPVCKEFXR 131

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RESULT      10
US-07-893-929A-5
; Sequence 5, Application US/07893929A
; Patent No. 533667
; GENERAL INFORMATION:
; APPLICANT: Kirby, Edward P.
; APPLICANT: Peng, Man-ling
; TITLE OF INVENTION: Alboaggregins: Platelet
; TITLE OF INVENTION: Agonists Bind To Platelet
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of The Common-
; ADDRESSEE: Wealth System of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 Inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/893,929A
; FILING DATE: 19920605
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/803,630
; FILING DATE: December 3, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TEXELX: NO. 5336667e
; INFORMATION FOR SEQ ID NO.: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-893-929A-5

Query Match          47.7%; Score 333.5; DB 1; Length 132;
Best Local Similarity 47.3%; Pred. No. 7.6e-34;
Matches    61; Conservative   24; Mismatches   35; Indels    9; Gaps     2

OY      3 ECPGSSWSDYRCYKPFQEMTWADAQRFCSQDAGHLLSVETALASVDNVLYANKE 62
       1 | | | | | : | | | : | | | | | | | | | | | | | | | | | | :
Db      1 DCPSSWSFKPYCYIVKELTKTMDAEKFCSEQANDGHILVTSIESYEAAVFVELLENVK 60
       1 | | | | | : | | | : | | | | | | | | | | | | | | | | | | :
OY      63 YLTRIWIIGLRYONNGGPC-----SSTSYENLV--DPEEGFMYSRDRRLREMFVDC 113
       1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 TTKYNWVGISLVONKEQQSCSEMDSGSXYHENLIKPNPKCKFLVKKESDFRTMSNVIC 120
       1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      114 QOHSPICKP 122
       1 | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 OKHIFMCKP 129

RESULT      11
PCT-US92-10344-5
; Sequence 5, Application PC/TUS9210344
; GENERAL INFORMATION:
; APPLICANT: Kirby, Edward P.
; APPLICANT: Peng, Man-ling
; TITLE OF INVENTION: Alboaggregins: Platelet

```

;; TITLE OF INVENTION: Agonists Which Bind To Platelet
;; TITLE OF INVENTION: Membrane Glycoprotein Ib
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Temple University - Of The Common-
;; ADDRESSEE: Health System of Higher Education
;; STREET: 406 University Services Building
;; CITY: Philadelphia
;; STATE: Pennsylvania
;; COUNTRY: U.S.A.
;; ZIP: 19122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: Wordperfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/10344
;; FILING DATE: 19921201
;; CLASSIFICATION:
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/803,630
;; FILING DATE: December 3, 1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Monaco, Daniel A.
;; REGISTRATION NUMBER: 30,480
;; REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-8383
;; TELEFAX: (215) 568-5549
;; TELEX: None
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 132 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
PCT-US92-10344-5

Query Match 47.7%; Score 333.5; DB 5; Length 132;
Best Local Similarity 47.3%; Pred. No. 7,66-34;
Matches 61; Conservative 24; Mismatches 35; Indels 9; Gaps 2;

QY 3 ECPSSGWSYDRYCYKPKQEMTADAFCSQAKGGHLSVETALASFPDNYVYANKE 62
DB 1 DCPSPDSSSEFYQCYQYKELKEDAEKFCSEQANDCHLVSIESYREAVFVALLSENVK 60

QY 63 YLTRYTWIGLRVONKQPC-----SSISYENLV--DPFCFMYSRDTRLREMFVDC 113
DB 61 TTKYVNWIGLGVONKKEQCSSEMSDSSSVXYENLIKRPKRCFVLKKESEFTWSNVYCE 120

QY 114 QOHSFICKF 122
DB 121 QKHIFWCKF 129

RESULT 12
US-07-893-929A-2
; Sequence 2, Application US/07893929A
; Patent No. 5336667
; GENERAL INFORMATION:
; APPLICANT: Kirby, Edward P.
; APPLICANT: Peng, Man-ling
; TITLE OF INVENTION: Alboaggregins: Platelet
; TITLE OF INVENTION: Agonists Which Bind To Platelet
; TITLE OF INVENTION: Membrane Glycoprotein Ib
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of The Common-
; ADDRESSEE: Health System of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania

;; COUNTRY: U.S.A.
;; ZIP: 19122
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: Wordperfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/893,929A
;; FILING DATE: 19920605
;; CLASSIFICATION: 435
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 07/803,630
;; FILING DATE: December 3, 1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Monaco, Daniel A.
;; REGISTRATION NUMBER: 30,480
;; REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-8383
;; TELEFAX: (215) 568-5549
;; TELEX: No. 5336667e
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 134 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
US-07-893-929A-2

Query Match 45.7%; Score 319.5; DB 1; Length 134;
Best Local Similarity 42.7%; Pred. No. 4,2e-32;
Matches 56; Conservative 27; Mismatches 39; Indels 9; Gaps 2;

QY 1 DLECPSSGWSYDRYCYKPKQEMTADAFCSQAKGGHLSVETALASFPDNYVYAN 60
DB 1 DFHCLPGMSAYDYCYKPFNEPKNWDARFCQKQADSGHLVSIETMGDAFVAQLISEN 60

QY 61 KEYLTRYTWIGLRVONKQPC-----SSISYENLVDPF--ECFMYSRDTRLREMFV 111
DB 61 IOSNEHYTWIGLRVONKKEQCSSEMSDSSSVXYENLIKRLMKRGALFQESGRKRWNLG 120

QY 112 CEQOHSFICKF 122
DB 121 CIOQLNPFWCKF 131

RESULT 13
PCT-US92-10344-2
; Sequence 2, Application PC/TUS9210344
; GENERAL INFORMATION:
; APPLICANT: Kirby, Edward P.
; APPLICANT: Peng, Man-ling
; TITLE OF INVENTION: Alboaggregins: Platelet
; TITLE OF INVENTION: Agonists Which Bind To Platelet
; TITLE OF INVENTION: Membrane Glycoprotein Ib
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of The Common-
; ADDRESSEE: Health System of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10344
; FILING DATE: 19921201

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2002, 16:23:36 ; Search time 16.24 Seconds

(without alignments)
745,521 Million cell updates/sec

Title: US-09-926-256-1

Perfect score: 699

Sequence: 1 DLECPGSMSTDRICRYKPKF.....WPKVDCEQQHSICKFTPR 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_71:*
2: pir1:*
3: pir2:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344.5	49.3	129	2	JC4329
2	323	46.2	133	2	A47267
3	314.5	45.0	152	2	JC4690
4	303.5	43.4	152	2	JC7134
5	296	42.3	144	2	PC7027
6	260.5	37.3	146	2	JC7135
7	254.5	36.4	131	2	JC5058
8	237.5	34.0	146	2	JC7105
9	230.5	33.0	123	2	B42972
10	208.5	29.8	125	2	JC5059
11	204.5	29.3	146	2	JC4691
12	203.5	29.1	125	2	B47267
13	191.5	27.4	123	2	JC2415
14	181	25.9	166	2	RGH01A
15	181	25.9	166	2	A45751
16	176.5	25.3	175	2	S29822
17	176	25.2	40	2	S56006
18	169.5	24.2	175	2	A41719
19	168	24.0	165	2	A47148
20	167.5	24.0	175	2	A37194
21	167	23.9	173	2	B47134
22	166.5	23.8	175	2	A49616
23	160	22.9	165	2	A28351
24	160	22.9	166	1	RGH01B
25	158	22.6	162	1	LNRC1
26	157	22.5	162	1	LNRC3
27	156	22.3	40	2	S56007
28	154	22.0	2415	1	A39086
29	153	21.9	174	2	S54979

30	151	21.6	2124	2	A28452	proteoglycan core
31	151	21.6	2132	1	A55182	aggrean precursor
32	147.5	21.1	912	2	A54423	brevican precursor
33	147	21.0	40	2	B56829	alboaggregin-B alp
34	146.5	21.0	883	2	S57653	brevican precursor
35	146.5	21.0	1463	2	A53210	phospholipase A2 r
36	146	20.9	1340	2	A39808	proteoglycan core
37	146	20.9	2327	2	T42630	aggrean - bovine
38	145.5	20.8	330	2	T46256	brevican - human (
39	145	20.7	1487	2	S48719	phospholipase-A(2)
40	144.5	20.7	883	2	S49126	brevican precursor
41	143	20.5	135	2	A38609	lectin, galactose-
42	140	20.0	2109	1	T50421	aggrean precursor
43	139.5	20.0	178	2	T29536	hypothetical prote
44	139	19.9	1268	2	S52781	neurocan - mouse
45	138	19.7	1257	2	S28764	neurocan precursor

ALIGNMENTS

RESULT 1

JC4329 coagulation factor IX-binding protein A chain - habu

C:Species: Trimeresurus flavoviridis (habu)

C>Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 13-Mar-1998

C:Accession: JC4329

R:Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.

J. Biochem. 118, 965-973, 1995

A:Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus f

A:Reference number: JC4329; MUID:96318509

A:Accession: JC4329

A:Molecule type: protein

A:Residues: 1-129 <ATO>

C:Comment: This protein binds calcium.

C:Superfamily: tetralectin; C-type lectin homology

C:Keywords: anticoagulant; blood coagulation; calcium binding; venom

F:2-127/Domain: C-type lectin homology <LCH>

F:2-13,30-127,102-119/Disulfide bonds: #status predicted

Query Match	Best Local Similarity	49.3%	Score 344.5	DB 2	Length 129
Matches 62; Conservative 24; Mismatches 33; Indels 9; Gaps 2;					
OY 3	ECPSGMSYDRYCYKPKFQEMTWADQRCSEBOAGCHLSVETALASFYDNVLYANKE 62				
DB 1	DQPSGMSYEGHCYKPKFLKXTWDAERFCTPOAGCHLVSTESAGDAFVAQLVTENIQ 60				
OY 63	YLTRVWIGLRVQNGQPC-----SSISTYBNLYDPPE--CFMVSQDTRLEMKRVDC 113				
DB 61	NTRSYWVWIGLRVQNGKQCSSEMSDSSSVSNWIEASKTCLEKTEGFRKWNIVYG 120				
OY 114	QOHSFICK 121				
DB 121	QONPVCE 128				
RESULT 2					
A47267	botrocetin alpha chain - jararaca				
N:Alternate names:	two chain botrocetin alpha chain				
C:Species:	Bothrops jararaca (Jararaca)				
C>Date:	21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998				
C:Accession:	A47267; B37958				
R:Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.					
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993					
A:Title:	Primary structure of two-chain botrocetin, a von Willebrand factor modulator				
A:Reference number:	A47267; MUID:93157385				
A:Accession:	A47267				
A:Molecule type:	protein				
A:Residues:	1-133 <USA>				
A:Experimental source:	venom				

A:Note: sequence extracted from NCBI backbone (NCBIP:124085)
R:Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sugita,
Biochemistry 30, 1957-1964, 1991
A:Title: Isolation and chemical characterization of two structurally and functionally di
A:Reference number: A37958; WUID:91129280
A:Accession: B37958
A:Molecule type: protein
A:Residues: 1-40 <FUJ>
C:Complex: heterodimer of alpha and beta (see PIR:B47267) chains
C:Superfamily: tetranectin; C-type lectin homology
C:Keywords: hemagglutinin; heterodimer; venom
F:2-128/Domin: C-type lectin homology <LCH>
F:2-13,30-118,103-120/Disulfide bonds: #status experimental
F:80/Disulfide bonds: Interchain (to beta-75) #status experimental

Query Match 46.2%; Score 323; DB 2; Length 133;
Best Local Similarity 46.6%; Pred. No. 2,9e+26;
Matches 62; Conservative 25; Mismatches 36; Indels 10; Gaps 3;

OY 3 ECPGSSSYDRYCYPFKQEMTWADAFRCSEQAAGKGLLSVET-ALEASFVNVLANK 61
:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
D 1 DCPGSSSYEGNCKYKFFQOKMNADEAFRCSEQAAGKGLLSIKYSKERDFVDLTKN 60
OY 62 EYLTRYIWGLRNQNGGPC-----SISYEINLYDF--ECFNVSRTRLREWRKVC 112
: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 61 QSSDLTAWIAGLRNEKECCSSSEMSDSSVSENVERTVKCFALDKLGFLVWNLTYC 120
OY 113 EQHSPICKETRP 125
:::|||
Db 121 AQKNPFVCKSP 133

RESULT 3
JC4690
coagulation factor IX/factor X-binding protein chain A precursor - habu
C:Species: Trimeresurus flavoviridis (habu)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000
C:Accession: JC4690; A39332
R:Matsumaki, R.; Yoshitane, E.; Yamada, M.; Shim, K.; Abode, H.; Morita, T.
Biochem. Biophys. Res. Commun. 220, 382-387, 1996
A:Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from s
A:Reference number: JC4690; WUID:96184662
A:Accession: JC4690
A:Molecule type: mRNA
A:Residues: 1-152 <MAT>
A:Cross-references: DDBJ:883331; NID:g1402639; PIDN:BAH11887.1; PID:g1402640
A:Experimental source: venom
R:Abode, H.; Hyuga, M.; Morita, T.
J. Biol. Chem. 266, 14903-14911, 1991
C:Title: The primary structure of coagulation factor IX/factor X-binding protein isolate
tein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.
A:Reference number: A39332; WUID:91332000
A:Accession: A39332
A>Status: preliminary
A:Molecule type: protein
A:Residues: 24-152 <ATO>
C:Superfamily: tetranectin; C-type lectin homology
C:Keywords: anticoagulant; blood coagulation; glycoprotein; hemolympn; lectin
F:1-23/Domin: signal sequence #status predicted <SIG>
F:2-152/Product: factor IX/X binding protein chain A #status predicted <MAT>
F:25-150/Domin: C-type lectin homology <LCH>
F:25-36,53-150,125-142/Disulfide bonds: #status predicted

Query Match 45.0%; Score 314.5; DB 2; Length 152;
Best Local Similarity 45.3%; Pred. No. 2,6e+25;
Matches 58; Conservative 26; Mismatches 35; Indels 9; Gaps 2;

OY 3 ECPGSSSYDRICYPFKQEMTWADAFRCSEQAAGKGLLSVETRLAEASFVNVLANK 62
:|||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
D 24 DCLSGSSYEGNCKYKFEKKWTMEDARVCTEQAKGAILVSISSGGEDFVAQLVQNMR 83

[illegible]

RESULT 4

agkiscutacin alpha chain precursor - sharp-nosed viper
 N:Alternate names: fibrinogenolytic venom protein
 C:Species: Agkistrodon acutus (Sharp-nosed Viper)
 C:Date: 04-Mar-2000 #sequence,revision 04-Mar-2000 #text,change 24-Oct-2000
 C:Accession: J07134; PC7037
 C:Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
 Biochem. Biophys. Res. Commun. 265, 530-535, 1999
 A:Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic ve
 A:Reference number: J07134; MUID:20025379
 A:Accession: J07134
 A:Molecule type: mRNA
 A:Residues: 1-152 <CHE>
 A:Cross-references: GB:AF176420
 A:Experimental source: venom gland
 A:Accession: PC7037
 A:Molecule type: protein
 A:Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>
 C:Superfamily: tetraonectin; C-type lectin homology
 C:Keywords: disulfide bond; heterodimer; venom
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-152/Product: agkiscutacin alpha chain #status experimental <MNT>

Query Match	43.48;	Score 303.5;	DB 2;	Length 152;
Best Local Similarity	44.58;	Pred. No. 3.5e-24;		
Matches 57; Conservative	24;	Mismatches 38;	Indels 9;	Gaps 2

QY 3

```

OY      3  ECPGSGSYDYBYCYKPKROEMTADARFCSEOKGHHLSVEFALPASTVDVYANKE  62
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      24  DCSGSGSYEGHCKYFKQKQKTADAPFCSTQKQNGHLSVSISSGADPVAHLLQKIK  83

OY      63  YLTFYIIMIGLRYNQKQPC-----SISYENLV--DPRECFSVSDTFLRPMFYKDE  113
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      84  SAKTHVIMIGLQAKQKOSTIEMSDGSSISTENWIEEBSKCLGVHITETGFHKNENFYCE  143

OY      114  QQHSFICK  121

Db      144  QODPEVCE  151

```

RESULT

aggretrin alpha/chain - Malayan pit viper (fragment)
 C,Species: Calloselasma rhodostoma (Malayan pit viper)
 C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
 C,Accession: PC7027
 R,Chung, C.H.; Au, L.C.; Huang, T.F.
 Biochem. Biophys. Res. Commun. 263, 723-727, 1999
 A,Title: Molecular cloning and sequence analysis of aggretrin, a collagen-like platelet
 A,Reference number: PC7027; MUID:99443731
 A,Accession: PC7027
 A:Molecule type: mRNA
 A:Residues: 1144<CHU>
 A:Experimental source: venom gland
 C:Superfamily: tetranectin; C-type lectin homology
 C:Keywords: disulfide bond; platelet aggregation; venom

Query Ma

Query Match	42.3%	Score 296	DB 2	Length 144
Best Local Similarity	43.8%	Pred. No.	2e-23	
Matches 57	Conservative 23	Mismatches	38	Indels 12
				Gaps 4

Oy	3	ECBCEGSSYURCYCCKPCKOCTMTAADQRCBQAKGHLLSVETLASEFVNDNYLYAKKE	62
	:	: : : : : : : : : : : : : :	:
Db	12	DCDGBMSPYDHOHCYAFNEBCKTWDCEAKFCRQENGAHLLASTIENSGEADFV-SWILISKD	70
Oy	63	YLT--RTWIGLGVAKGQPC-----SSISEYENYD--PPECFMVSRDRLREMEKVD	111
	:		:
Db	71	ELADEDEYVWIGLRAKNEQDCSSMSDSSSVSTENLLDLTKKCGALEKLGFRKRWNYT	130
Oy	112	GEODHSFICK	121
	:	: :	:
Db	131	GEOMHAEVCK	140

RESULT 6
JC7135
agkissactacin beta chain precursor - sharp-nosed viper
N:Alternate names: fibrinogenlytic venom protein
C:Species: Agkistrodon acutus (Sharp-nosed viper)
C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000
C:Accession: JC7135; PC7038
R:Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.-Y.; Zhang, M.; Liu, J.
Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A:Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom
A:Reference number: JC7134; M0ID:20025379
A:Accession: JC7135
A:Molecule type: mRNA
A:Residues: 1-146 <CHE>
A:Cross-references: GB:AF176421
A:Experimental source: venom gland
A:Experimental source: venom gland
A:Molecule type: PC7038
A:Molecule type: protein
A:Residues: 24-50;59-83;102-107;112-114 <CH2>
C:Superfamily: tetranectin; C-type lectin homology
C:Keywords: disulfide bond; heterodimer; venom
F:1-23/Domains: signal sequence #status predicted <SIG>
F:24-146/Product: agkissactacin beta chain #status experimental <MAT>

	Query Match	37.3%	Score 260.5:	DB 2:	Length 146:
	Best Local Similarity	43.2%:	Pred. No. 9.7e-20:		
	Matches 54:	Conservative 21:	Mismatches 41:	Indels 9:	Gaps 5:
Oy	3 ECPSSGSSYDRCYKPFKEQEMTWADAPFCSEQAQGHLLSETALAEAFVNDVLYANKE	62			
	: : : : :				
Dd	24 DCPSSMSIEGHCYCFFPDEPKTMALAKFCTQHKGSHLSRSEADFV--VILTPFS	81			
Oy	63 VLTFRYIWIGLR-VQN---KGOPCISISYLEVPDECFMRSRDTRLRFEMFKVDCEQHS	117			
	: : : : :				
Dd	82 LKTDLWIGLKINMGCYWKMSDGRKLDYRKDWREDFEC-LYSR-TVNNEMLSMDGGTCS	139			
Oy	118 FICKF 122				
	:				
Dd	140 FVCKF 144				

```

RESULT 7
JC5058
bitiscetin alpha chain - puff adder
N:Alternate names: von Willebrand factor modulator protein
C:Species: Bitis arietans (puff adder)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 12-Feb-1999
C:Accession: JC5058, JC5916
R:Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Ozaki, Y.
submitted to JIPID, January 1997
A:Description: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor
A:Reference number: JC5058
A:Contents: snake venom
A:Accession: JC5058
A:Molecule type: protein
A:Residues: 1-131 <MAT>
A:Experimental source: snake venom
R:Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Ozaki, Y.
Comm. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997

```

A:Title: Complete amino acid sequence of bitisetin, a novel von Willebrand factor modulator
A:Reference number: JCS916
A:Accession: JCS916
A:Molecule type: protein
A:Residues: 1-131 <MA2>
A:Experimental source: venom
A:Comment: This protein is a modulator of a von Willebrand factor modulator.
C:Superfamily: tetraneectin; C-type lectin homology
C:Keywords: venom
C:4-125/Domain: C-type lectin homology <LCH>

[illegible]

```

RESULT      8
JC7105
aggrelin beta chain - Malayan pit viper
C:Species: Calloselasma rhodostoma (Malayan pit viper)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C:Accession: JC7105
R:Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A:Title: Molecular cloning and sequence analysis of aggrelin, a collagen-like platelet
A:Reference number: PC7027; MUID:99443731
A:Accession: JC7105
A:Molecule type: mRNA
A:Residues: 1-146 <CHU>
A:Experimental source: venom gland
C:Superfamily: tetraneurin; C-type lectin homology
C:Keywords: disulfide bond; platelet aggregation; venom

```

Query Match	34.0%	Score 237.5	DB 2:	Length 146:
Best Local Similarity	38.6%	Pred. No. 2,4e-17:		
Matches 49:	Conservative 19:	Mismatches 46:	Indels 13:	Gaps 5
QY	3	ECPCGMSYDRCYKPFCKEMTWADQRCFSQAKGHLISVETALAEAFVNVLYANKE	62	
	:	:	:	:
DB	24	DCCPSGMSSTEGCIKYPFNEPKNMADDERCKIQPKHSHLSVQSAAEAFV--VKLTRR	81	
QY	63	YLTRITGLRYONKQGPC-----SSISYENLVDPFEFCFVSRDTRLREMFKYDCEQ	115	
	:	:	:	:
DB	82	EKANLYVMGL--SNIIWGCNMQMSDQARLNYKDMQDQSPSC-LAFRGVH-TWELNMDSSST	137	
QY	116	HSFICKF 122		
	:	:		
DB	138	CSFVCKF 144		

RESULT 9
BA2972
coagulation factor x activating enzyme (EC 3.4.24.-) light chain - Russell's viper
C.Species: *Vipera russelli* (Russell's viper)
C.Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C.Accession: BA2972
R.Takaya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, T.; Biol. Chem. 267, 14109-14117, 1992
A.Title: Coagulation factor x activating enzyme from Russell's viper venom (RVV-X). A

A:Note: sequence extracted from NCBI backbone (NCBI:P:124086)
R:Fujimura, Y.; Tifani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sugita, K. *Journal of Biological Chemistry* 273, 1557-1564, 1998
B:Biochemistry 30, 1557-1564, 1991
A:Title: Isolation and chemical characterization of two structurally and functionally different lectins from the venom of the scorpion *Uroctonus*
A:Reference number: A37958; PMID:91129280
A:Accession: C37958
A:Molecule type: protein
A:Residues: 1-40 <FU>
C:Complex: heterodimer of alpha (see PIR:A47267) and beta chains
C:Superfamily: tetraneurin; C-type lectin homology
C:Keywords: hemagglutinin; heterodimer; venom
F:2-121/Domain: C-type lectin homology <LCH>
F:2-13-30-121_98-113/Disulfide bonds: #status experimental
F:75/Disulfide bonds: interchain (to alpha-80) #status experimental

Query Match	Score	DB 2,	Length
Best Local Similarity	29.18;	203.5;	125;
Matches 47; Conservative	35.98;	Pred. No. 6.7e-14;	
	26;	Mismatches 39;	Indels 19; Gaps 8;

QY 3 ECPGSESYRBYCYCKPKPKROKMTADARFCSEAKGGHILLSVEALPLASVDVNTYANKE 62
 1 DCPFDMSYSEHCCTREFKEMHHMDAAEEFCITDQCAHLVSFSQKEADYRSL--TSE 57
 63 YLT-RTYIWIGLR-VONKGQPC-----SSISYEN-LVDFEFCFMYSRDTRLREMKVD 111
 58 MKQDVMYIGISLVQWVK---CRFEMTDGMEFDYDYLLIAYEAE-VASKPTLN-NKMWIIP 112
 QY

QY	112	CEQHSFICKF	122
		: : : :	
Db	113	CTRFKNFVCEF	123

RESULT **13**

JC2415
echicetlin beta chain - saw-scaled viper
C/Species: Echiscarinatus (saw-scaled viper)
C/Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 15-Oct-1996
C/Accession: JC2415
R/Peng, M.; Holt, J.C.; Niewiarowski, S.
Biochem. Biophys. Res. Commun. 205, 68-72, 1994
A>Title: Isolation, characterization and amino acid sequence of echicetlin beta subunit,
A/Reference number: JC2415; MUID:95091801
A/Accession: JC2415
A/Molecule type: protein
A/Residues: 1-123 <PEN>

A:Experimental source: venom
C/Comment: This protein inhibits aggregation of fixed platelets induced by several platelet agonists such as ADP, epinephrine, collagen, thrombin, and arachidonic acid.
I/Ilebrand factor and albosagregins.
C/Superfamily: tetranectin; C-type lectin homology
C/Keywords: anticoagulant; dimer
F/2-119/Domain: C-type lectin homology <LCH>
F/2-119/Disulfide bonds: #status predicted

Query Match	27.4%	Score 191.5;	DB 2;	Length 123;
Best Local Similarity	31.2%;	Pred. No. 1.2e-12;		
Matches 39; Conservative	24;	Mismatches 49;	Indels 13;	Gaps 4;

[illegible]

QY	117	SEICK	121
		1:11	
Db	116	YFVCK	120

RESULT 14

RGHUL1A

regenerating islet lectin 1-alpha precursor [validated] - human
 N:Alternate names: lithostathine; pancreatic thread protein (PTP); reg I protein; reg
 N:Contains: pancreatic stone protein (PSP)

C.Date: 31-Mar-1990 #sequence_revision 03-Aug-1995 #text_change 08-Dec-2000
C.Accession: A35197, B28351, S12950, S02767, S02419, S00113, S01471, A252466
R.Watanabe, T.; Yonekura, H.; Terazono, K.; Yamamoto, H.; Okamoto, H.

A:Title: Complete nucleotide sequence of human reg gene and its expression in normal product of the gene.
 2:Reference number: A35197; MUID:90237042

A: Molecule type: DNA
A: Residues: 1-166 <WAT>

A:Cross-references: GB:J05412
R:Terzono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Oka
J. Biol. Chem. 263, 2111-2114, 1988

A:Title: A novel gene activated in regenerating islets.
A:Reference number: A92704; MUID:8115343
A:Accession: B28351

A: Molecule type: mRNA
A: Residues: 1-166 <TER>
A: Cross-references: GB:M18963; NID:g190978; PID:M36558.1; PID:g190979

A: Title: Isolation and characterization of human reg protein produced in Saccharomyce
 B: Reference number: 810694
 C: Date: 1990-07-01
 D: Author(s): Iizuka, H.; Naito, T.; Yeraoka, H.; Matsumoto, K.; Yoshida, N.; Yeraoka
 E: Journal title: FEBS Lett.
 F: Volume: 272
 G: Issue: 85-88
 H: Pages: 1990

A:Reference Name: S12950; MOLID:21052149
A:Accession: S12950
A:Molecule type: protein
A:Residues: 23-52:160-166 <TM>

A1>Note: sequence determined from protein isolated after human cDNA sequence was clone
Ride Caro, A.M.; Adich, Z.; Fournet, B.; Capon, C.; Bonicel, J.J.; de Caro, J.D.; Ro
Bichim. Biophys. Acta 994. 281-284. 1989

A:Title: N-terminal sequence extension in the glycosylated forms of human pancreatic
A:Reference number: S02767; MUID:89150292
A:Accession: S02767

A;Molecule type:protein
A;Residues: 23-47 <DEC>
R;Routimi, P.; de Caro, J.; Bonicel, J.; Rovery, M.; de Caro, A.

FEBIS Lett. 229, 171-174, 1988
A:Title: The disulfide bridges of the immunoreactive forms of human pancreatic stone
.:Reference number: S02419; MUID:88152214

A:Accession: S02419
A:Molecule type: protein
A:Residues: 63-72;125-139;150-157;160-166 <R0U>

A: Note: disulfide bonds
R: de Caro, A.M.; Bonicelli, J.J.; Rouimi, P.; de Caro, J.D.; Sarles, H.; Rovey, M.
Eur. J. Biochem. 168, 201-207, 1987

A:Title: Complete amino acid sequence of an immunoreactive form of human pancreatic s
A:Reference number: S00113; MUID:88029417
A:Accession: S00113

A: Molecule type: protein
A: Residues: 34-166
R: Rouimi, P.; Bonicel, J.; Rovey, M.; de Caro, A.

FEBS Lett. 216:193-199, 1987
A:Title: Cleavage of the Arg-116 bond in the native polypeptide chain of human pancre
Reference number: S01471; MUID:87219142

A:Accession: S014/1
A:Molecule type: protein
A:Residues: 33-48 <R02>
B:Source: C. botulinum T. Wolfson
C:Database: W. Campbell
D:Ref: H. De Groot
E:Pubmed: 10101010

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 3, 2002, 16:25:11 ; Search time 11.83 Seconds
(without alignments)
412.398 Million cell updates/sec

Title: US-09-926-256-1
Perfect score: 699
Sequence: 1 DLECPGWSYDRYCYRPFK.....WFKYDCQHSFICKTRPR 126

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349.5	50.0	133	1 RHCA_AGRH	P81397 agkistrodon
2	338.5	48.4	131	1 ABAL_TRIAB	P81111 trimeresuru
3	323	46.2	133	1 BOTR_BOTJA	P22029 bothrops ja
4	322.5	46.1	132	1 ABBA_TRIAB	P81115 trimeresuru
5	318.5	45.6	134	1 ABA2_TRIAB	P81112 trimeresuru
6	316.5	45.3	129	1 RHCA_AGRH	P81398 agkistrodon
7	314.5	45.0	152	1 IXA_TRIEL	P23806 trimeresuru
8	264.5	37.8	123	1 ABA4_TRIAB	P81114 trimeresuru
9	264.5	37.8	133	1 ECHA_ECHCA	P81017 echis carin
10	203.5	29.4	125	1 ABA3_TRIAB	P81113 trimeresuru
11	204.5	29.3	146	1 IXB_TRIEL	P23807 trimeresuru
12	203.5	29.1	125	1 BOTR_BOTJA	P22030 bothrops ja
13	191.5	27.4	123	1 ECHB_ECHCA	P81996 echis carin
14	187.5	26.8	118	1 ABBA_TRIAB	P81116 trimeresuru
15	181	25.9	166	1 LIRA_HUMAN	P05451 homo sapien
16	176.5	25.3	175	1 PAP1_MOUSE	P35230 mus musculu
17	169.5	24.2	175	1 PAP1_RAT	P25031 rattus norv
18	168	24.0	165	1 LITH_MOUSE	P43137 mus musculu
19	167.5	24.0	175	1 LITH_BOVIN	P23132 bos taurus
20	167	23.9	173	1 LIT2_MOUSE	P08731 mus musculu
21	166.5	23.8	175	1 PAP1_HUMAN	P06141 homo sapien
22	160	22.9	165	1 LITH_RAT	P10758 rattus norv
23	160	22.9	166	1 LITH_HUMAN	P48304 homo sapien
24	157	22.5	162	1 LEC3_MEGRO	P07439 megabalanus
25	154	22.0	161	1 PCGA_MEGRO	P16112 homo sapien
26	153	21.9	174	1 PAP3_RAT	P42854 rattus norv
27	151	21.6	2124	1 PCGA_RAT	P07897 rattus norv
28	151	21.6	2132	1 PCGA_MOUSE	P61282 mus musculu
29	150	21.5	174	1 PAP3_MOUSE	P09049 mus musculu
30	147.5	21.1	912	1 PCGB_BOVIN	P28062 bos taurus
31	146.5	21.0	175	1 PCGB_HUMAN	P09278 homo sapien
32	146.5	21.0	883	1 PCGB_MOUSE	P61361 mus musculu
33	146.5	21.0	1463	1 PA2R_BOVIN	P49259 bos taurus

34	146	20.9	2364	1 PCGA_BOVIN	P13608 bos taurus
35	144.5	20.7	883	1 PCGB_RAT	P55068 rattus norv
36	143	20.5	135	1 LEC3_CROAT	P21963 crataeus att
37	140	20.0	2109	1 PCGA_CHICK	P07898 gallus gall
38	139	19.9	1268	1 PCGN_MOUSE	P55066 mus musculu
39	138	19.7	1257	1 PCGN_RAT	P55067 mus musculu
40	134	19.2	147	1 LEC3_ANTCR	P06027 anthocidari
41	134	19.2	2333	1 PCGA_CANFA	P28343 canis fami
42	133.5	19.1	1458	1 PA2R_RABIT	P49260 oryctolagus
43	132.5	19.0	172	1 LEC3_PLEMA	P03988 pleurodeles
44	132.5	19.0	175	1 PAP2_MOUSE	P09037 mus musculu
45	131	18.7	122	1 LITH_PIG	Q29191 sus scrofa

ALIGNMENTS

RESULT 1
RHCA_AGRH STANDARD: PRT; 133 AA.
AC P81397:
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Rhodocetin alpha subunit.
OS Agkistrodon rhodostoma (Malayan pit viper) (Callisela rhodostoma).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scieroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Callisela.
OX NCBI TaxID=8717;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Wang R, Kini M, Chung M.C.M.;
RL Submitted (JUN-1998) to the SWISS-PROT data bank.
CC -I- SUBUNIT: HETEROTRIMER OF TWO ALPHA SUBUNITS AND ONE BETA SUBUNIT.
CC -I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
DR HSSP; P23806; 11XX.
DR InterPro; IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c.1.
DR SMART; SMO0034; CLECT.1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
DR Venom; Lectin.
KW DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
FT DISULFD 2 13 BY SIMILARITY.
FT DISULFD 30 127 BY SIMILARITY.
FT DISULFD 102 119 BY SIMILARITY.
SQ SEQUENCE 133 AA: 15962 MW: 386EAC519DFC674D CRC64;

Query Match 50.0%; Score 349.5; DB 1; Length 133;
Best Local Similarity 48.1%; Pred. No. 4,6e-30;
Matches 64; Conservative 24; Mismatches 36; Indels 9; Gaps 2;

QY 3 ECPGWSYDRYCYRPFKEQMTADQRFCSQANGHLISVETALASVDNYANKE 62
DB 1 DCPDMSSTKSYCRPFKEKTEBEARCTQEKRAHLSMENRLEAVFYVMENNE 60
QY 63 YLRIYIWLGRQNNQGPC-----SSISYENLVDPF--ECFMVSRDRLRMFVND 113
DB 61 NKIYRWGLKLENGQSRNLEMSDSSISYENLYPEYKCFMDHQSLPMWADCE 120
QY 114 QHNSFICKTRPR 126
DB 121 EKNVMECKFOLPR 133

RESULT 2
ABAL_TRIAB STANDARD: PRT; 131 AA.
ID ABAL_TRIAB
AC P81111;
DT 15-JUL-1998 (Rel. 36, Created)

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DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Albogagreglin A subunit 1.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Albogagreglin A and B. Structure and interaction with human
platelets."
RT Thromb. Haemost. 79:609-613(1998).
RL -1- FUNCTION: BINDS TO PLATELET GPIIb/III RECEPTOR SYSTEM AND STIMULATES
AGGUTINATION.
CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4,
CC DISULFIDE-LINKED.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
DR HSSP; P23806; IIX.
DR InterPro: IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
KM Venom; Lectin. 1 129 C-TYPE LECTIN (LONG FORM).
FT DOMAIN 2 13 BY SIMILARITY.
FT DISULFID 30 127 BY SIMILARITY.
FT DISULFID 102 119 BY SIMILARITY.
FT DISULFID 131 AA; 15427 MW; B3569F5BP91F6624 CRC64;
SQ SEQUENCE 131 AA; 15427 MW; B3569F5BP91F6624 CRC64;

Query Match 48.4%; Score 338.5; DB 1; Length 131;
Best Local Similarity 47.3%; Pred. NO. 6.5e-29;
Matches 62; Conservative 21; Mismatches 39; Indels 9; Gaps 2;

QY 3 ECPSSGSSYGRYCKPKPKQEMTWADQRFCSQAKGHLISYETALASFDVNLVANK 62
DB 1 DCPSSMSYDGYCYKRVKRIQTIWEDAEKRFCSQANDGHLVIESAGEAFVYOLVSENIR 60
QY 63 YLTRFYWIGLRVQKKGQPC-----SSISYENLVDP--PFCFNVSRDTRLREMFVDC 113
DB 61 SEKHYYWIGLRVQKKGQCSSEMSDGSVVDNLQENKTRKCYGLEKRAEFRTWSNVYCG 120
QY 114 QQHSFICKFTR 124
DB 121 HEYFVCKFKR 131

RESULT 3
BOTA_BOTJA STANDARD; PRT: 133 AA.
ID BOTA_BOTJA
AC P22029;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Botrocetin, alpha chain (Platelet coagglutinin).
OC Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN
RP SEQUENCE. AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=93157385; PubMed=8430107;
RA Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
RA Titani K.;
RT "Primary structure of two-chain botrocetin, a von Willebrand factor

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RT modulator purified from the venom of Bothrops jararaca.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
RN
RP SEQUENCE OF 1-40.
RC TISSUE=Venom;
RX MEDLINE=91129280; PubMed=1993206;
RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
RA Fukui H., Sugimoto M., Ruggieri Z.M.;
RT "Isolation and chemical characterization of two structurally and
functionally distinct forms of botrocetin, the platelet coagglutinin
isolated from the venom of Bothrops jararaca.";
RL Biochemistry 30:11957-11964(1991).
CC -1- FUNCTION: TWO-CHAIN BOTROCETIN FORMS AN ACTIVATED COMPLEX WITH
CC VWF, AND THE COMPLEX THEN BINDS TO PLATELET GPIIb, RESULTING IN
CC PLATELET AGGUTINATION.
CC -1- FUNCTION: THERE ARE TWO DISTINCT FORMS OF THE VON WILLEBRAND
CC FACTOR-DEPENDENT PLATELET COAGGLUTININ. THE DIMERIC FORM IS
CC 34-TIMES MORE ACTIVE THAN THE ONE-CHAIN BOTROCETIN IN PROMOTING
CC VWF BINDING TO PLATELETS.
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF AN ALPHA AND A BETA CHAIN.
CC VWF AND BOTROCETIN FORM A SOLUBLE COMPLEX.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
DR PIR; B37958; B37958.
DR PIR; A47267; A47267.
DR HSSP; P23806; IIX.
DR InterPro: IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
KM Venom; Lectin. 2 13
FT DISULFID 30 128 INTERCHAIN (WITH C-75 IN BETA CHAIN).
FT DISULFID 80 80
FT DISULFID 103 120
SQ SEQUENCE 133 AA; 15215 MW; E4CF4502946AC74B CRC64;

Query Match 46.2%; Score 323; DB 1; Length 133;
Best Local Similarity 46.6%; Pred. NO. 2.9e-27;
Matches 62; Conservative 25; Mismatches 36; Indels 10; Gaps 3;

QY 3 ECPSSMSYDRYCYKPFQKQEMTWADQRFCSQAKGHLISYET-ALASFDVNLVANK 61
DB 1 DCPSSMSYEGYCYKPFQKQMWADAEKRFCSQAKGHLISYIKYKQFVDDLVKNT 60
QY 62 YLTRFYWIGLRVQKKGQPC-----SSISYENLVDP--ECFNVSRDTRLREMFVDC 112
DB 61 QSSDIYAMIGLRVENKKEKQCSSEMSDGSVYENVYRYKKCFALKDGLFVIMNLVYC 120
QY 113 EQQHSFICKFTR 125
DB 121 AQKNFVCKSP 133

RESULT 4
ABBA_TRIAB STANDARD; PRT: 132 AA.
ID ABBA_TRIAB
AC P81115;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Albogagreglin B alpha subunit.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,

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Db 121 FLCKFPKP 128

RESULT 7
ID IXA_TRIPL STANDARD; PRT: 152 AA.

DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Coagulation factor IX/factor X-binding protein A chain precursor
DE (IX/X-BP).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_Taxid=88087;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=6184662; PubMed=8645314;
RA Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
RT "CDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
RT protein from snake venom."
RL Biochem. Biophys. Res. Commun. 220:382-387(1996).
[2]
RP SEQUENCE OF 24-152.
RX MEDLINE=9133200; PubMed=1831197;
RA Atoda H., Hyuga M., Morita T.;
RT "The primary structure of coagulation factor IX/factor X-binding
RT protein isolated from the venom of Trimeresurus flavoviridis.
RT Homology with asialoglycoprotein receptors, proteoglycan core
RT protein, tetranectin, and lymphocyte Fc epsilon receptor for
RT immunoglobulin E."
RL J. Biol. Chem. 266:14903-14911(1991).
RN [3]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RA MEDLINE=9731317; PubMed=9187649;
RA Mizuno H., Fujimoto Z., Kojizumi M., Kano H., Atoda H., Morita T.;
RT "Structure of coagulation factors IX/X-binding protein, a heterodimer
RT of C-type lectin domains".
RL Nat. Struct. Biol. 4:438-441(1997).
CC -1- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND
CC FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.
CC -1- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
CC -1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
CC -----
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CC or send an email to license@slb-slb.ch).
CC -----
CC EMBL: D83331; BAA1887.1; .
DR PIR: A39332; A39332.
DR PDB: 1IXX; 06-MAY-98.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KW Prosite; Calcium; Signal; 3d-structure.
FT SIGNAL 1 23
FT CHAIN 24 152
FT COAGULATION FACTOR IX/FACTOR X-BINDING
FT PROTEIN A CHAIN.
FT DOMAIN 24 152
FT C-TYPE LECTIN (LONG FORM).
FT DISULFID 25 36
FT BY SIMILARITY.
FT DISULFID 53 150
FT BY SIMILARITY.
FT DISULFID 102 102
FT INTERCHAIN (WITH C-98 OF B CHAIN).

FT DISULFID 125 142 BY SIMILARITY.
SQ SEQUENCE 152 AA; 17213 MW; FB3DD2369009263 CRC64;

Query Match 45.0%; Score 314.5; DB 1; Length 152;
Best Local Similarity 45.3%; Pred. No. 2.6e-26;
Matches 58; Conservative 26; Mismatches 35; Indels 9; Gaps 2;

QY 3 ECPGWSYDRYCYKPKFOEMTWADQRFCSQOANGHLLSVETALEASFVDNYLTKKE 62
D :|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db DCLGWSSEYEGHCYKAFKFKYTWEDAEKRYCTQAKGAHLVSISSSEADFFVQLVYQNMK 83
QY 63 YLTFTYTWGLRVQNGKGPC-----SSISTYENIVDPFE--CFMSRDRLRKRWVDE 113
| :|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 84 RLDTYTWGLRVQNGKVCQNSSEMSDSSVSYTENWIEBSKTLGLKEKDFRKWVNYTCG 143
QY 114 QQHSFKC 121
| :|:|:
Db 144 QQNPVCE 151

RESULT 8
ID IXA_TRIAB STANDARD; PRT: 123 AA.
AC P81114;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Albogagregin A subunit 4.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_Taxid=8765;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom.
RX MEDLINE=96189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calveze J.J., Niewiarowski S.;
RT "Albogagregin A and B. Structure and interaction with human
RT platelets."
RL Thromb. Haemost. 79:609-613(1998).
CC -1- FUNCTION: BINDS TO PLATELET GPIIb/IX RECEPTOR SYSTEM AND STIMULATES
CC AGGUTINATION.
CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4,
CC DISULFIDE-LINKED.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
CC HSSP: P23807; 11XX.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KW Venom; Lectin.
FT DOMAIN 1 121
FT DISULFID 2 13
FT DISULFID 30 119
FT DISULFID 96 111
FT BY SIMILARITY.
SQ SEQUENCE 123 AA; 14365 MW; DACFBEI219C9B1E CRC64;

Query Match 37.8%; Score 264.5; DB 1; Length 123;
Best Local Similarity 40.5%; Pred. No. 3.9e-21;
Matches 53; Conservative 23; Mismatches 34; Indels 21; Gaps 6;

QY 3 ECPGWSYDRYCYKPKFOEMTWADQRFCSQOANGHLLSVETALEASFVDN---VLY 58
:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 1 DCPEDWSSEYEGHCYKAFKFKYTWEDAEKRYCTQAKGAHLVSISSSEADFFVQLVYQNMK 60
QY 59 ANKEYLRYTWIGLRVQNGKGPCSS-----ISTYENIVDPFEKMSVSDTFLREKFKVD 111
| :|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db 61 AN-----LWVIGL--SNLMQCNQSWSDGTLYLDKXWKEQFEC-LVSRFTN-NEWLSMD 110

OY 112 CEOHSHFICKF 122
 DB 111 CSSTHSFVCEP 121

RESULT 9
 ECHA_ECHCA STANDARD; PRT; 133 AA.

AC P81017;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Echicetin alpha subunit.
 OS Echis carinatus (Saw-scaled viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Echis.
 NCBI_TaxID=40353;

RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=97250657; PubMed=9163349;
 RA Polgar J., Magneat E.M., Peltsch M.C., Wells T.N.C., Sagi M.S.A.,
 RA Clemetson K.J.;
 RT "Amino acid sequence of the alpha subunit and computer modelling of
 RT carinatus (saw-scaled viper).";
 RT Biochem. J. 323:533-537(1997).

CC CHARACTERIZATION.
 CC TISSUE=Venom;
 CC MEDLINE=93244424; PubMed=8481512;
 CC Pong M., Lu W., Bevilacqua L., Niewiarowski S., Kirby E.P.;
 CC "Echicetin: a snake venom protein that inhibits binding of von
 CC Willebrand factor and alphaaggregins to platelet glycoprotein IIb/IIIa";
 CC Blood 81:2321-2328(1993).
 CC -1- FUNCTION: BINDS TO PLATELET GPIIb AND INHIBITS PLATELET
 CC AGGUTINATION.
 CC -1- SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC HSSP: P23806; I1XX.
 CC InterPro: IPR001304; lectin_c.
 CC Pfam: PF000059; lectin_c; 1.
 CC SMART: SM00034; CLECT; 1.
 CC PROSITE: PS00615; C-TYPE LECTIN_1; FALSE_NEG.
 CC PROSITE: PS50041; C-TYPE LECTIN_2; 1.

DR Venom; Lectin.
 KM DISULFID 4 15 BY SIMILARITY.
 FT DISULFID 31 127 BY SIMILARITY.
 FT DISULFID 102 119 BY SIMILARITY.
 FT DISULFID 81 81 INTERCHAIN (WITH C-75 IN BETA CHAIN) (BY
 FT SIMILARITY).
 SO SEQUENCE 133 AA; 15803 MW; 8F1IC2DBDC70B16 CRC64;

Query Match 37.8%; Score 264.5; DB 1; Length 133;
 Best Local Similarity 37.8%; Pred. NO. 4.3e-21;
 Matches 51; Conservative 32; Mismatches 41; Indels 11; Gaps 4;

OY 1 DLPCSGMSYDRCYKPFKOEMTWADQRCSEQAKGHLISYETALAEAFVNVLYAN 60
 DB 1 DQDLSGMSYEGCYOUFLRK-TWDEAKYCN-QMDGHLVSTESNAKAEEFVAQLIRK 58
 OY 61 --KEYLRYIWIIGLRVONKGOPC-----SSISYENLVDFECFVMSRDTLRLEWFKYD 111
 DB 59 LPKSAIDRWVIGLRDRSKRCQGLMTWNSFVYEHVVPPTKCFVLERQTEFRKVIAYN 118
 OY 112 CEOHSHFICKFTRPR 126
 DB 119 CEKFPVCAKIPR 133

RESULT 10
 ABA3_TRIAB STANDARD; PRT; 125 AA.

AC P81113;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Alboaggregin A subunit 3.
 OS Trimeresurus albolabris (White-lipped pit viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Chordata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 NCBI_TaxID=8765;

RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=98189535; PubMed=9531050;
 RA Kovalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
 RA Calvete J.J., Niewiarowski S.;
 RT "Alboaggregins A and B. Structure and interaction with human
 RT platelets";
 RT Thromb. Haemost. 79:609-613(1998).
 CC -1- SUBUNIT: BINDS TO PLATELET GPIIb/IIIa RECEPTOR SYSTEM AND STIMULATES
 CC AGGUTINATION.
 CC -1- FUNCTION: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4,
 CC DISULFIDE-LINKED.
 CC HSSP: P23807; I1XX.
 CC InterPro: IPR001304; lectin_c.
 CC Pfam: PF000059; lectin_c; 1.
 CC SMART: SM00034; CLECT; 1.
 CC PROSITE: PS00615; C-TYPE LECTIN_1; FALSE_NEG.
 CC PROSITE: PS50041; C-TYPE LECTIN_2; 1.

DR Venom; Lectin.
 KM DOMAIN 3 123 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 4 15 BY SIMILARITY.
 FT DISULFID 32 121 BY SIMILARITY.
 FT DISULFID 98 113 BY SIMILARITY.
 SO SEQUENCE 125 AA; 14798 MW; CAFA24C098DF3293 CRC64;

Query Match 29.4%; Score 205.5; DB 1; Length 125;
 Best Local Similarity 33.9%; Pred. NO. 6.7e-15;
 Matches 43; Conservative 24; Mismatches 47; Indels 13; Gaps 5;

OY 3 ECPSCGMSYDRCYKPFKOEMTWADQRCSEQAKGHLISYETALAEAFVNVLYANKE 62
 DB 3 DCPFGMSYEGCYVYNNKMMWDAESRCROHRSYVSHSGEVDVFSKTFPIIR 62
 OY 63 YLTRYIWIIGLRVONKGOPCSS-----ISYENLVDFECFVMSRDTLRLEWFKYDCQO 115
 DB 63 Y-DEVWML--SDIWKECTKEMSDGARLDYKAWSGSKSYC-LVSKYTN-NEWLSMDCSRT 116
 OY 116 HSFICKF 122
 DB 117 RYPCVCKF 123

RESULT 11
 IXB_TRIFL STANDARD; PRT; 146 AA.

AC P23807; Q91247;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Coagulation factor IX/factor X-binding protein B chain precursor
 DE (IX/X-BP).
 OS Trimeresurus flavoviridis (Habu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Chordata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 NCBI_TaxID=88087;
 [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=96184662; PubMed=8645314;
 RA Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
 RT "cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
 RT protein from snake venom.";
 RL Biochem. Biophys. Res. Commun. 220:382-387(1996).
 RN [2]
 (2) SEQUENCE OF 24-146.
 RC TISSUE=Venom;
 RX MEDLINE=91332000; PubMed=1831197;
 RA Atoda H., Hyuga M., Morita T.;
 RT "The primary structure of coagulation factor IX/factor X-binding
 RT protein isolated from the venom of *Trimeresurus flavoviridis*.
 RT Homology with asialoglycoprotein receptors, proteoglycan core
 RT protein, tetranectin, and lymphocyte Fc epsilon receptor for
 RT immunoglobulin E.";
 RL J. Biol. Chem. 266:14903-14911(1991).
 RN [3]
 (3) X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=97331317; PubMed=9187649;
 RA Mizuno H., Fujimoto Z., Koltzumi M., Kano H., Atoda H., Morita T.;
 RT "Structure of coagulation factors IX/X-binding protein, a heterodimer
 RT of C-type lectin domains.";
 RL Nat. Struct. Biol. 4:438-441(1997).
 CC -1- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND
 CC FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.
 CC -1- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
 CC -1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
 CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: D83332; BAA11888.1; -
 CC DR PIR: B39332; B39332.
 CC DR PIR: 11XX; 06-MAY-98.
 CC DR InterPro: IPR001304; lectin_c.
 CC DR Pfam: PF00059; lectin_c; 1.
 CC DR SMART: SM00034; CLECT; 1.
 CC DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
 CC DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
 CC DR Lectin; Calcium; Signal; 3D-structure.
 CC FT SIGNAL 1 23
 CC FT CHAIN 24 146 COAGULATION FACTOR IX/FACTOR X-BINDING
 CC FT DOMAIN 24 144 PROTEIN B CHAIN.
 CC FT DISULFID 25 144 C-TYPE LECTIN (LONG FORM).
 CC FT DISULFID 53 142 BY SIMILARITY.
 CC FT DISULFID 98 98 INTERCHAIN (WITH C-102 OF A CHAIN).
 CC FT DISULFID 119 134 BY SIMILARITY.
 CC FT DISULFID 146 134 BY SIMILARITY.
 CC SQ SEQUENCE 146 AA; 16922 MM; 8E1961C59F657C CRC64;

Query Match 29.3%; Score 204.5; DB 1; Length 146;
 Best Local Similarity 33.9%; Pred. No. 1e-14;
 Matches 43; Conservative 23; Mismatches 48; Indels 13; Gaps 4;

QY 3 ECPSSGSSYDRYCKRPFKEQMTWADAQRCSEDAKGGHLLSVETALASVDVNLVANK 62
 DB 24 DCPDMSWSEYEGHCYKPFSEPKWMDAENFCTQOHAGHLLVFSQSEADFFV--VKLAF 81
 QY 63 YLTPYTWIGLAVOKKQGPC-----SSISYENLVDPFECFMYSRDTRLREWFKVDCEQ 115
 DB 82 FGHISIFWGL--SNVWNOCMOMNAALRYKAMAE--ESYCYFSTNNKWRACRAM 137
 QY 116 HSFICKF 122
 DB 138 AQFVCEF 144

RESULT 12
 BOTB_BOTVA STANDARD: PRT: 125 AA.
 AC P22030;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Botrocelin, beta chain (platelet coagglutinin).
 OS Botrotops jararaca (jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Bothrops.
 NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE=Venom;
 RX MEDLINE=93157385; PubMed=8430107;
 RA Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
 RA Titani K.;
 RT "Primary structure of two-chain botrocelin, a von Willebrand factor
 RT modulator purified from the venom of *Bothrops jararaca*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
 RN [2]
 RP SEQUENCE OF 1-40.
 RC TISSUE=Venom;
 RX MEDLINE=91129280; PubMed=1993206;
 RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
 RA Fukui H., Sugimoto M., Ruggeri Z.M.;
 RT "Isolation and chemical characterization of two structurally and
 RT functionally distinct forms of botrocelin, the platelet coagglutinin
 RT isolated from the venom of *Bothrops jararaca*.";
 RL Biochemistry 30:1957-1964(1991).
 CC -1- FUNCTION: TWO-CHAIN BOTROCELIN FORMS AN ACTIVATED COMPLEX WITH
 CC VWF, AND THE COMPLEX THEN BINDS TO PLATELET GPIB, RESULTING IN
 CC PLATELET AGGUTINATION.
 CC -1- FUNCTION: THERE ARE TWO DISTINCT FORMS OF THE VON WILLEBRAND
 CC FACTOR-DEPENDENT PLATELET COAGULOTININ. THE DIMERIC FORM IS
 CC 34-TIMES MORE ACTIVE THAN THE ONE-CHAIN BOTROCELIN IN PROMOTING
 CC VWF BINDING TO PLATELETS.
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF AN ALPHA AND A BETA CHAIN.
 CC VWF AND BOTROCELIN FORM A SOLUBLE COMPLEX.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC DR PIR: C37958; C37958.
 CC DR PIR: B47267; B47267.
 CC DR HSSP: P23807; 11XX.
 CC DR InterPro: IPR001304; lectin_c.
 CC DR Pfam: PF00059; lectin_c; 1.
 CC DR SMART: SM00034; CLECT; 1.
 CC DR PROSITE: PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
 CC DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
 CC DR Venom; Lectin.
 CC FT DISULFID 2 13
 CC FT DISULFID 30 121 INTERCHAIN (WITH C-80 IN ALPHA CHAIN).
 CC FT DISULFID 75 75
 CC FT DISULFID 98 113
 CC SQ SEQUENCE 125 AA; 15037 MM; 1ED2027ED817FCA0 CRC64;

Query Match 29.1%; Score 203.5; DB 1; Length 125;
 Best Local Similarity 35.9%; Pred. No. 1.1e-14;
 Matches 47; Conservative 26; Mismatches 39; Indels 19; Gaps 8;

QY 3 ECPSSGSSYDRYCKRPFKEQMTWADAQRCSEDAKGGHLLSVETALASVDVNLVANK 62
 DB 1 DCPDMSWSEYEGHCYKPFSEPKWMDAENFCTQOHAGHLLVFSQSEADFFV--TS 57
 QY 63 YLT-RYIWIGL-RVOKKQGPC-----SSISYEN-LVDPFECFMYSRDTRLREWFKVD 111
 DB 58 MLKGVWVWIGLSDVWNR--CRFETDGMEDYDDYLLAEVRC-VASKPTLN-NKMWIIP 112
 QY 112 CEQHSFICKF 122

Db 113 CTRKNCVCEP 123

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RESULT 13
ID ECHB_ECHCA STANDARD; PRT; 123 AA.
AC P81996;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Echicetin beta subunit.
OS Echis carinatus (Saw-scaled viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Echis.
OX NCBI_TaxID=40353;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=95091801; PubMed=7999097;
RA Peng M., Holt J.C., Niewiarowski S.;
RT "Isolation, characterization and amino acid sequence of echicetin beta
RT subunit, a specific inhibitor of von Willebrand factor and thrombin
RT interaction with glycoprotein Ib."
RL Biochem. Biophys. Res. Commun. 205:68-72(1994).
RN [2]
RP SEQUENCE OF 1-30.
RC TISSUE-Venom;
RX MEDLINE=97250657; PubMed=9163349;
RA Polgar J., Maguenat E.M., Peltsch M.C., Wells T.N.C., Saqi M.S.A.,
RA Clemetson K.J.;
RT "Amino acid sequence of the alpha subunit and computer modelling of
RT the alpha and beta subunits of echicetin from the venom of Echis
RT carinatus (Saw-scaled viper)."
RL Biochem. J. 323:533-537(1997).
RN [3]
RP CHARACTERIZATION.
RC TISSUE-Venom;
RX MEDLINE=93244424; PubMed=8481512;
RA Peng M., Lu W., Bevilgia L., Niewiarowski S., Kirby E.P.;
RT "Echicetin: a snake venom protein that inhibits binding of von
RT Willebrand factor and alphaagregins to platelet glycoprotein Ib."
RL Blood 81:2321-2328(1993).
CC -1- FUNCTION: BINDS TO PLATELET GPIIb AND INHIBITS PLATELET
CC AGGLUTINATION.
CC -1- SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
DR HSP: P23807; IIX.
DR Interpro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
KM Venom: Lectin.
FT DOMAIN 1 121 C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 119 BY SIMILARITY.
FT DISULFID 75 75 INTERCHAIN (WITH C-81 IN ALPHA CHAIN) (BY
FT SIMILARITY).
FT DISULFID 96 111 BY SIMILARITY.
SQ SEQUENCE 123 AA; 14869 MW; C42C0AD7CD18CA6 CRC64;

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Query Match 27.4%; Score 191.5; DB 1; Length 123;
 Best Local Similarity 31.2%; Pred. No. 2e-13;
 Matches 39; Conservative 24; Mismatches 49; Indels 13; Gaps 4;

QY 4 CPSPGSSYDRYCYKPKPEQMTWADAFRCSEQAKGHLISVETALEASFDVNLVYANKY 63
 DB 2 CLPDMSTYEGCTKIVFERANWADAEFCMKQYVDGHLVSRNSKEVDPMISLAFPMIK- 60
 QY 64 LTRYIWIGLRVONKGPC-----SSISYENLVDPFECFVNSDTRLREMFKVCDEQOH 116

Db 61 -MELWVIGL--SDYWRDCYEWMSDGAQLDYKAMDNBRHCF--AAKTTDQNMRRKCSGEF 115
 QY 117 SFICK 121
 Db 116 YFVCK 120

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RESULT 14
ID ABBT_TRIAB STANDARD; PRT; 118 AA.
AC P81116;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last sequence update)
DE Alboaggregin B beta subunit.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvele J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
RT platelets."
RL Thromb. Haemost. 79:609-613(1998).
CC -1- FUNCTION: BINDS TO PLATELET GPIIb/IX RECEPTOR SYSTEM AND STIMULATES
CC AGGLUTINATION.
CC -1- SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS. DISULFIDE-LINKED.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
DR HSP: P23807; IIX.
DR Interpro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
KM Venom: Lectin.
FT DOMAIN 1 118 C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 75 75 INTERCHAIN (WITH C-79 IN ALPHA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 96 111 BY SIMILARITY.
SQ SEQUENCE 118 AA; 13794 MW; 059EDF6B474C4CE CRC64;

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Query Match 26.8%; Score 187.5; DB 1; Length 118;
 Best Local Similarity 33.3%; Pred. No. 5e-13;
 Matches 41; Conservative 18; Mismatches 53; Indels 11; Gaps 4;

QY 3 ECPSPGSSYDRYCYKPKPEQMTWADAFRCSEQAKGHLISVETALEASFDVNLVYANKY 62
 Db 1 DCPSPGSSYDRYCYKPKPEQMTWADAFRCSEQAKGHLISVETALEASFDVNLVYANKY 60
 QY 63 YLTRYI-----WIGLRVQ-NKGQPCSSISYENLVDPFECFVNSDTRLREMFKVCDEQOH 116
 Db 61 XXXXWIGLTVDSACRLQWSDG---TTLKSNAMWTAESSEC--IAKTTDQNMWTRSCSRTY 115
 QY 117 SFI 119
 Db 116 PFV 118

RESULT 15
 LITR_HUMAN STANDARD; PRT; 166 AA.
 ID LITR_HUMAN
 AC P05451; P11379;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Lithostathine I alpha precursor (Pancreatic stone protein) (PSP)
DE (Pancreatic thread protein) (PTP) (Islet of Langerhans regenerating
DE protein) (REG) (Regenerating protein I alpha) (Islet cells
DE regeneration factor) (ICRF).
GN REGIA OR REG OR PSPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=88115343; PubMed=2963000;
RA Terazono K., Yamamoto H., Takasawa S., Shiga K., Yonemura Y.,
RA Tochino Y., Okamoto H.;
RT "A novel gene activated in regenerating islets.";
RL J. Biol. Chem. 263:2111-2114(1988).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=90237042; PubMed=2332435;
RA Matanabe T., Yonekura H., Terazono K., Yamamoto H., Okamoto H.;
RT "Complete nucleotide sequence of human reg gene and its expression in
RT normal and tumoral tissues. The reg protein, pancreatic stone
RT protein, and pancreatic thread protein are one and the same product
RT of the gene.";
RL J. Biol. Chem. 265:7432-7439(1990).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=89292148; PubMed=2525567;
RA Giordani D., Bernard J.-P., Rouquier S., Iovanna J., Sarrles H.,
RA Dagorn J.-C.;
RT "Secretory pancreatic stone protein messenger RNA. Nucleotide
RT sequence and expression in chronic calcifying pancreatitis.";
RL J. Clin. Invest. 84:100-106(1989).
RN [4]
RN SEQUENCE OF 34-166.
RX MEDLINE=88029417; PubMed=3655916;
RA de Caro A.M., Bonicel J.J., Rouini P., de Caro J.D., Sarrles H.,
RA Rovey M.;
RT "Complete amino acid sequence of an immunoreactive form of human
RT pancreatic stone protein isolated from pancreatic juice.";
RL Eur. J. Biochem. 168:201-207(1987).
RN [5]
RN SEQUENCE OF 34-98.
RX MEDLINE=87099950; PubMed=3541906;
RA Montalto G., Bonicel J.J., Multigner L., Rovey M., Sarrles H.,
RA de Caro A.M.;
RT "Partial amino acid sequence of human pancreatic stone protein, a
RT novel pancreatic secretory protein.";
RL Biochem. J. 238:227-232(1986).
RN [6]
RN SEQUENCE OF 34-78.
RX MEDLINE=86086356; PubMed=3908481;
RA Gross J., Carlson R.I., Brauer A.W., Margolies M.N., Warshaw A.L.,
RA Wands J.R.;
RT "Isolation, characterization, and distribution of an unusual
RT pancreatic human secretory protein.";
RL J. Clin. Invest. 76:2115-2125(1985).
RN [7]
RN SEQUENCE OF 23-47.
RX MEDLINE=89150292; PubMed=2493268;
RA de Caro A.M., Adrich Z., Fournet B., Capon C., Bonicel J.J.,
RA de Caro J.D., Rovey M.;
RT "N-Terminal sequence extension in the glycosylated forms of human
RT pancreatic stone protein. The 5-oxoproline N-terminal chain is O-
RT glycosylated on the 5th amino acid residue.";
RL Biochim. Biophys. Acta 994:281-284(1989).
RN [8]
RN SEQUENCE OF 33-58.
RX MEDLINE=87219142; PubMed=3108036;
RA Rouini P., Bonicel J.J., Rovey M., de Caro A.;
RT "Cleavage of the Arg-Ile bond in the native polypeptide chain of
RT human pancreatic stone protein.";
RN FEBS Lett. 216:195-199(1987).
RN [9]
RN IDENTITY OF REG WITH PSP.
RX MEDLINE=89350859; PubMed=2764894;
RA Stewart T.A.;
RT "The human reg gene encodes pancreatic stone protein.";
RL Biochem. J. 260:622-623(1989).
RN [10]
RN DISULFIDE BONDS.
RX MEDLINE=91032149; PubMed=2226837;
RA Itoh T., Tsuzuki H., Katoh T., Teraoka H., Matsumoto K., Yoshida N.,
RA Terazono K., Matanabe T., Yonekura H., Yamamoto H., Okamoto H.;
RT "Isolation and characterization of human reg protein produced in
RT Saccharomyces cerevisiae.";
RL FEBS Lett. 272:85-88(1990).
RN [11]
RN ALZHEIMER'S DISEASE AND DEVELOPMENTAL EXPRESSION REGULATION.
RX MEDLINE=90368981; PubMed=2394826;
RA de la Monte S.M., Ozturk M., Wands J.R.;
RT "Enhanced expression of an exocrine pancreatic protein in Alzheimer's
RT disease and the developing human brain.";
RL J. Clin. Invest. 86:1004-1013(1990).
RN [12]
RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=96256285; PubMed=8654365;
RA Bertrand J.A., Pignol D., Bernard J.-P., Verdier J.-M., Dagorn J.-C.,
RA Fontecilla-Camps J.C.;
RT "Crystal structure of human lithostathine, the pancreatic inhibitor
RT of stone formation.";
RL EMBO J. 15:2678-2684(1996).
RN [13]
RN X-RAY CRYSTALLOGRAPHY (1.30 ANGSTROMS) OF 23-166.
RX MEDLINE=20092874; PubMed=10625646;
RA Gerbaud V., Pignol D., Loret E., Bertrand J.A., Verdier J.M.,
RA Fontecilla-Camps J.C., Canseller J.P., Gabas N., Verdier J.M.;
RT "Mechanism of calcite crystal growth inhibition by the N-terminal
RT undecapeptide of lithostathine.";
RL J. Biol. Chem. 273:1057-1064(2000).
RN [14]
RN STRUCTURE BY NMR OF 34-166.
RX MEDLINE=97120677; PubMed=8961348;
RA Patard L., Stoven V., Charib B., Bontems F., Lallemand J.-Y.,
RA de Reggi M.;
RT "What function for human lithostathine? structural investigations by
RT three-dimensional structure modeling and high-resolution NMR
RT spectroscopy.";
RL Protein Eng. 9:949-957(1996).
RN [15]
RN FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM
RN CARBONATE PRECIPITATION. MAY BE ASSOCIATED WITH NEURONAL
RN SPROUTING IN BRAIN, AND WITH BRAIN AND PANCREAS REGENERATION.
RN [16]
RN TISSUE SPECIFICITY: IN PANCREATIC ACINAR CELLS AND, IN LOWER
RN LEVELS, IN BRAIN.
RN [17]
RN DEVELOPMENTAL STAGE: HIGH EXPRESSION LEVELS IN FETAL AND INFANT
RN BRAINS; MUCH LOWER IN ADULT BRAINS.
RN [18]
RN DISEASE: ALZHEIMER'S DISEASE AND DOWN'S SYNDROME PATIENTS SHOW
RN ENHANCED EXPRESSION OF PSP-RELATED TRANSCRIPTS AND INTRANEURONAL
RN ACCUMULATION OF PSP-LIKE PROTEINS IN THEIR BRAINS.
RN [19]
RN SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
RN [20]
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RN between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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RN or send an email to license@sib-sib.ch).
RN [21]
RN EMBL: M27189; AAA60546.1; -;
RN EMBL: M27189; AAA60545.1; -;
RN EMBL: M1963; AAA36558.1; -;
RN EMBL: J05412; AAA36559.1; -;
RN PIR: A25246; A25246.
RN PIR: B28351; B28351.

D	b	24	DCLGQWSSYINFCVGPFLKLTMTDEAERFCTEQAGNGLHVSFEASREADFVAGVLESENK	83
O	y	63	YLTRYIWTIGLRVNKGQPCSS-----ISVENLVDPR--ECFMVSRDTRLREMFKVDC	113
D	b	84	-IKPVMYIGTLRQNCGQQCSSKMSDSSRVSYENLVPEFSKKCFVLKDTGFRTWENVYCG	142
O	y	114	QOHSPICKFTFRPR	126
D	b	143	LKHVFMCXYLKPR	155
R	E	2	PRT; 157 AA.	
A	C	09YGC9	PRELIMINARY;	
D	T	01-MAY-1999	(TREMBlrel. 10, Created)	
D	T	01-MAY-1999	(TREMBlrel. 10, Last sequence update)	
D	T	01-DEC-2001	(TREMBlrel. 19, Last annotation update)	
D	E	MAUUSIGLIN ALPHA PRECURSOR,		
O	S	Agristrodon halays blomhoffi (Mamushi) (loydus blomhoffii).		
O	S	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
O	C	Leptodosteus; Squamata; Scleroglossa; Serpentes; Colubroidae;		
O	X	Viperidae; Crotalinae; Agkistrodon.		
R	N	NCBI TaxID=61300;		
R	N	SEQUENCE FROM N.A.		
R	X	MEDLINE=96319530; PubMed=9657448;		
R	A	Sakurai Y., Fujimura Y., Kokubo T., Imanura K., Kawasaki T., Handa M., Suzuki M., Matsui T., Titani K., Yoshida A.;		
R	T	"The cDNA cloning and molecular characterization of a snake venom platelet glycoprotein Ib-binding protein, mamushigin, from Agristrodon halays blomhoffii venom.";		
R	L	Thromb. Haemost. 79:1199-1207(1998).		
D	R	HSSP; P23806; iXX.		
D	R	InterPro: IPRO01304; lectin_c.		
D	R	Pfam; PF00059; lectin_c; 1.		
D	R	SMART; SM00034; CLECT; 1.		
D	R	PROSITE; PS00615; C-type_LECTIN_1; 1.		
K	M	signal.		
F	T	signal.		
S	O	SEQUENCE 157 AA; 18333 MW; 47DAAL17891CE1865 CRC64;		
Q	y	1 DLECPSGMSVDRVCYKRFKEOMETADARFCSEDAKGGSHLSVEFLAEASFVDNYLAN	60	
D	b	24 DSDDCSDMSSNGRCFYKLFOQAKMWADAERFCTEORTGAHLVISSTNEATAVNWISEN	83	
Q	y	61 KEYLTRYTWIGLRVNKGOPC-----SISYENDLVDPR--FECFMVSRDTRLREMFKYD	111	
D	b	84 IK-KRDYVWIGLTGVNEGQCKSRMSDRSSVSYSYENDLVPMNSKKCVLKEYEGSRKMENVY	142	
Q	y	112 CEQHSHFTCKFTFRPR	126	
D	b	143 CGQKYYAFMCKFLRPR	157	
R	E	3	PRT; 142 AA.	
A	C	09PSM6	PRELIMINARY;	
D	T	01-MAY-2000	(TREMBlrel. 13, Created)	
D	T	01-MAY-2000	(TREMBlrel. 13, Last sequence update)	
D	T	01-JUN-2001	(TREMBlrel. 17, Last annotation update)	
D	E	PLATELET GLYCOPROTEIN IB-BINDING PROTEIN ALPHA SUBUNIT, GPIB-BP ALPHA SUBUNIT.		
O	S	Bohrops jararaca (Jararaca);		
O	C	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

[illegible]

OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Deinagkistrodon.
 OX NCBI_TaxID=36307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM;
 RA Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,
 RA Liu J.;
 RA "Aggiscutacin, a new fibrinolytic & anti-platelet protein from
 RT Agkistrodon acutus venom.";
 RT Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF176421; AAF26287.1; -
 DR HSSP: P23807; I1XX.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 SQ SEQUENCE 146 AA; 16726 MW; 7360B6D6864131BB CRC64;

Query Match 37.4%; Score 261.5; DB 13; Length 146;
 Best Local Similarity 43.2%; Pred. No. 1.7e-21;
 Matches 54; Conservative 21; Mismatches 41; Indels 9; Gaps 5;

QY 3 ECPGSSSYDRCYKPFQEMTWADAQRCSBOAKGHLSTALEAFVNDVLYANKE 62
 DB 24 DCPSSMSYEGHCYKPFDEKTMADAEKFTQOHGSHLSFHSSEADVFV--VTLTTPS 81
 QY 63 YLTTRYTWIGLR-VQN-----KGPCSSISYENLVDPFECFVNSRDTRLREFKVDCOOHS 117
 DB 82 LKTDLVWIGLKNMGCKYKMSDGTKLDKYKDMREGEFC-LVSR-TYVNNENLSMDCGTTCS 139
 QY 118 FICKF 122
 DB 140 FVCKF 144

RESULT 11
 093427 PRELIMINARY; PRT; 148 AA.
 AC 093427;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CONVULXIN BETA PRECURSOR.
 GN CVX BETA.
 OS Crotalus durissus terrificus (South American rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 OX NCBI_TaxID=8732;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 24-53; 99-109 AND 126-145.
 RC TISSUE=VENOM GLAND;
 RA MEDLINE=98524901; PubMed-9657980;
 RA Leduc M., Bon C.;
 RA "Cloning of subunits of convulxin, a collagen-like platelet-
 RT aggregating protein from Crotalus durissus terrificus venom.";
 RT Biochem. J. 333:389-393(1998).
 CC -1- FUNCTION: BINDS TO THE PLATELET AND COLLAGEN RECEPTOR,
 CC GLYCOPROTEIN VI (GPVI).
 CC -1- SUBUNIT: HETEROHETEROMER OF THREE ALPHA CHAINS AND THREE BETA
 CC CHAINS.
 CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
 DR EMBL: Y16349; CAA76182.1; -
 DR HSSP: P23807; I1XX.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.

DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 KW Venom; Lectin; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 148
 FT DOMAIN 26 146
 FT DISULFID 26 26
 FT DISULFID 27 38
 FT DISULFID 55 144
 FT DISULFID 100 100
 FT DISULFID 121 136
 FT SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC6539BF CRC64;

Query Match 37.4%; Score 261.5; DB 13; Length 148;
 Best Local Similarity 42.1%; Pred. No. 1.7e-21;
 Matches 53; Conservative 18; Mismatches 42; Indels 13; Gaps 5;

QY 4 CPGSSSYDRCYKPFQEMTWADAQRCSBOAKGHLSTALEAFVNDVLYANKE 63
 DB 27 CPGSSSYDRCYKPFQEMTWADAQRCSBOAKGHLSTALEAFVNDVLYANKE 84
 QY 64 LTRYTWIGLRVQNKGPC-----SSISYENLVDPFECFVNSRDTRLREFKVDCOOH 116
 DB 85 KSTFWIGL--ANNIMNCKMGMQSDGTREYKEMWEHEFC-LISR-TFDNOMLSARCSOTY 140
 QY 117 SFICKF 122
 DB 141 SFVCKF 146

RESULT 12
 091AM1 PRELIMINARY; PRT; 135 AA.
 AC 091AM1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE AGKISACTYACIN A CHAIN.
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Deinagkistrodon.
 OX NCBI_TaxID=36307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM;
 RA Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,
 RA Liu J.;
 RA "Aggiscutacin, a new fibrinolytic & anti-platelet protein from
 RT Agkistrodon acutus venom.";
 RT Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF176420; AAF26286.1; -
 DR EMBL: AF176420; AAF26286.1; -
 DR HSSP: P23806; I1XX.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c; 1.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 SQ SEQUENCE 135 AA; 15041 MW; F9A55A3802AFA291 CRC64;

Query Match 37.3%; Score 260.5; DB 13; Length 135;
 Best Local Similarity 49.0%; Pred. No. 1.9e-21;
 Matches 47; Conservative 19; Mismatches 23; Indels 7; Gaps 1;

QY 3 ECPGSSSYDRCYKPFQEMTWADAQRCSBOAKGHLSTALEAFVNDVLYANKE 62
 DB 24 DCPSSMSYEGHCYKPFQEMTWADAQRCSBOAKGHLSTALEAFVNDVLYANKE 83
 QY 63 YLTTRYTWIGLRVQNKGPC-----SSISYENLVDP 91
 DB 84 SAKIHWIGLRQNKKEKCSISWSDGSSISYENWIE 119

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RESULT 13
O9PSM9 PRELIMINARY; PRT; 131 AA.
ID O9PSM9
AC O9PSM9
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ECLV IX/X-BP ALPHA SUBUNIT=COAGULATION FACTOR IX/FACTOR X-BINDING
DE PROTEIN ALPHA SUBUNIT.
OC Echinocardium (Saw-scaled viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Echis.
OC NCBI_TaxID=40353;
RN [1]
RP MEDLINE=96196635; PubMed=8611513;
RX Chen Y.L., Tsai I.H.;
RT "Functional and sequence characterization of coagulation factor
RT IX/factor X-binding protein from the venom of Echis carinatus
RT leucogaster."
RL Biochemistry 35:5264-5271(1996).
DR HSP; P23806; IXX.
DR Interpro: IPR001304; lectin_c.
DR Pfam: PR00059; lectin_c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 131 AA; 15439 MW; B85E6C5CBF317E24 CRC64;

Query Match 35.0%; Score 244.5; DB 13; Length 131;
Best Local Similarity 34.6%; Pred. No. 1.1e-19;
Matches 45; Conservative 27; Mismatches 47; Indels 11; Gaps 3;

OY 3 ECPSGMSSYDRYCYKPKFQKQEMTADQRFCSQAKGHLSEVTALEASFDVNLVYANK 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DCLPGMSSHGCHCKYKFNKEMKDAERFKQKQKSHLVSESEEGDFVAKLISENLE 60
OY 61 KELTRIVIGLRVQNKQPC-----ISYE--NLVDPECFMVSQDTLRERFKVD 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 KSHSIDVWVWGLYKGRWKQCSSEMSDGSKITRYQWKQKQPKCLGLEKQTEPRKWNLY 120
OY 112 CEOQHSFICK 121
:|||||:
DB 121 CEERQRTCE 130

RESULT 14
O9I840 PRELIMINARY; PRT; 146 AA.
ID O9I840
AC O9I840
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE AGGREGTIN BETA CHAIN (FRAGMENT).
OC Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Calloselasma.
OC NCBI_TaxID=8717;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=VENOM GLAND;
RX MEDLINE=9443731; PubMed=10512747;
RX Chung C.H., Au L.C., Huang T.F.;
RT "Molecular cloning and sequence analysis of aggretin, a collagen-like
RT platelet aggregation inducer."
RL Biochem. Biophys. Res. Commun. 263:723-727(1999).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE=VENOM GLAND;
RA Chung C.H., Au L.C., Huang T.F.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF244901; AAF79953.1; -.
DR HSP; P23807; IXX.
DR Interpro: IPR001304; lectin_c.
DR Pfam: PR00059; lectin_c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
FT NON_TER 146
SQ SEQUENCE 146 AA; 16770 MW; 930839140CFD8908 CRC64;

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Query Match 34.0%; Score 237.5; DB 13; Length 146;
Best Local Similarity 38.6%; Pred. No. 7.9e-19;
Matches 49; Conservative 19; Mismatches 46; Indels 13; Gaps 5;

OY 3 ECPSGMSSYDRYCYKPKFQKQEMTADQRFCSQAKGHLSEVTALEASFDVNLVYANK 62
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 24 DCPGMSSEHGCHCKYKFNKEMKDAERFKLQPKHSLVFSQSAEADVF--VKLTRR 81
OY 63 YLRVYVIGLRVQNKQPC-----SSISYENLVDPPECFMVSQDTLRERFKVDCQO 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 82 LKANLVMMGL--SNIMGCGNQMWDGARLNKQMOESEC-LAFRGVH-TWMLNDCSST 137
OY 116 HSFICKF 122
:|||||
DB 138 CSFYCKF 144

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RESULT 15
O90WL9 PRELIMINARY; PRT; 124 AA.
ID O90WL9
AC O90WL9
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE AKITONIN (FRAGMENT).
OC Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OC NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RX Zha X.D., Xu K.S.;
RT "An Anticoagulant Protein From Venom of Agkistrodon acutus."
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF387100; AAK69351.1; -.
FT NON_TER 1
SQ SEQUENCE 124 AA; 14658 MW; 38D3F0BFE3AADAFC CRC64;

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Query Match 32.8%; Score 229.5; DB 13; Length 124;
Best Local Similarity 39.7%; Pred. No. 5.1e-18;
Matches 50; Conservative 24; Mismatches 43; Indels 9; Gaps 5;

OY 2 LECPGMSYDRYCYKPKFQKQEMTADQRFCSQAKGHLSEVTALEASFDVNLVYANK 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MDCPSDMSSEYGCNYLVVKEKKTWAEAKFCTEQRKEHLVSFHSAEVDFVASTFPIL 60
OY 62 EYLRVYVIGLR-VQN---KGQPCSSISYENLVDPPECFMVSQDTLRERFKVDCQO 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 SY--DLVWIGLKINWNGCYKRWSDGKLDYDKWREQFIC-LVSR-TVNNEMLSMDCGTT 116
OY 117 SFYCKF 122
:|||||
DB 117 SFVCEF 122

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Search completed: October 3, 2002, 16:28:44

• Fri Oct 4 08:20:13 2002

Job time: 233 sec

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